

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACCGCGTCCGGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTCGGTCTTCCCG
CAGCGCTACCCGCCATGCGCTGCCGCCGGCGCTGGGCTCCTGCCGCTTGCTG
CTGCTGCCGCCGCCGGAGGCCAAAGAACGCGACGCCCTGCCACCAGGTGCCGGGGCT
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAACGAACTTGGCGCGGGAAACA
CGGCTTGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC
CTGGAGGGCTGTGCAGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCAGAACCTACGGTCCCAGTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA
GGGCGACGGGTCTGCCGGTGCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGAAACGAGAACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCCGGCGAGTGTGAAGTGGCTGGGTGCT
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCCGGCGAGCCGCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGAGATGTGGACGAGTGCTCACTAGCAGAAAAAACCTGTGAGGAAAAACG
AAAATGCTACAATACTCCAGGGAGCTACGTCTGTGTGTGCCTGACGGCTTCGAAGAACG
GAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGCAAGACCTGTAATTGTGCCGGACTTACCCCTTAAATTATTAGAAGGATGTCC
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTGTCCCTTAAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTTGTATATTTGATAACAGTTCTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAGAAC
TTGGCCGCCATGGCCAACTTGTTATTGCAGCTATAATGGTTACAAATAAGCAATAGCA
TCACAAATTTCACAAATAAGCATTTCACTGCATTCTAGTTGTGGTTGTC
ATCAATGTATCTTATCATGTCTGGATCGGAATTAATTGGCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTTCTGAGGCGGAAGAAC
CAGCTGTGGAATG
TGTGTCAAGTTAGGGTGTGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAEEKTILSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKCCSPGTYPDCLACQGGSQRPCSG
NGHCSGDGSRQGDGSCRCHMGYQGPLCTCMDGYFSSLRNETHSICTACDESCKTCGTLNRDCGECEVGWLDE
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSVGCTGEGPGNCKECISGYAREHGQCADVDEC SLAEKT
CVRKNENCYNTPGSYVCVPDGFEETEDACVPPAEAEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAACTCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACCGTCCGCCAGGCCGGGAGGCAGCGGCCAGCCGTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCAGGTTGCCTAGGTGCG
GCACGAGGAGTTTCCCAGCAGCGAGGAGGTCTGAGCAGCATGGCCGGAGGAGCGCCCTC
CCTGCCGCCGCTCTGGCTCTGGAGCATCCTCTGTGCCTGACTGGCACTGCAGGGCGGAGGC
CGGGCCGCCGAGGAGGAGGCCTGTACCTATGGATCGATGCTCACCAAGGAAAGAGTACTCA
TAGGATTGAAGAAGATACTCTGATTGTTCAGAGGGAAAATGGCACCTTACACATGAT
TTCAGAAAAGCGAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTCAC
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGTCTTGCGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGAAACAGTGCCTCACAGGCA
TCAGTTGTTCAAGTTGGTTCCCATGTCTTGGAAAACAGGATGGGTGGCAGCATTGAAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAATGCTATCT
TCTTAAACATGTCAACAAGCTGAGTGCCAGGCCGGTGGCAGGAAATGGAGGCTTGTAAAT
GAAAGACGCATCTGCGAGTGTCTGATGGGTCCACGGACCTCACTGTGAGAAAGCCCTTG
TACCCACGATGTATGAATGGTGACTTGTGACTCCTGGTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAACCTGTGACAAAGCAAACGCTCAACCACCTGCTTAATGGAGGGACC
TGTTCCTACCCCTGGAAAATGTATTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCACAACCCTGCGAAATGGAGGTAATGCATTGGTAAAAGCAAATGTAAGTGT
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGCTGCGAGCCTGGCTGGTGACAT
GGAACCTGCCATGAACCCAAACAAATGCCATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCCAGCTCAGGCAGC
ACACGCCTTCACCTAAAAAGGCCAGGAGCGGGATCCACCTGAATCCAATTACATCTGG
TGAACCTCGACATCTGAAACGTTAAGTTACACCAAGTTACAGCCTTGTAAACCTTCA
TGTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGGCCTGAATTATTAGCT
TCATTATAAAATCACTGAGCTGATATTACTCTTCAAGTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTCTTGTTCAGTGTGTTGGACAGATTATATTATGTCAATTGA
TCAGGTTAAAATTTCAGTGTGAGTTGGCAGATATTCTAAAATTACAATGCATTATGGT
GTCTGGGGGCAGGGAAACATCAGAAAGTTAAATTGGCAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTCAAGATTATTGTCAGATATTAGAT
GTTTGTACATTAAAATTGCTCTTAATTAAACTCTCAATAACATATAATTGGCACC
TTACCATTATTCCAGAGATTCACTGAGGAAATTACACTGTGGTAGTGGCATT
AAACAATATAATATATTCTAAACACAATGAAATAGGAAATATAATGTATGAACCTTGCAT
TGGCTTGAAGCAATATAATATTGTAACAAAACACAGCTCTTACCTAATAAACATT
ACTGTTGTATGTATAAAATAAAGGTGCTGCTTAGTTTTGGAAAAAAA
AAAAAAAAAAAAAAAAGGGCGGCCGCACTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCCAACTGTTATTGCAGCTTATAATG

FIGURE 4

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T) : 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPHEKEALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKICPPGLEGEQCEISKCPQPCRNGGKICGSKCKCSKGYQGDLCSPKVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW
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Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGGCGTGGCGTCCGGCGGTCCAGAGGCCAGGAGGCGGAGGCCGGCAGCCTGG
CCCCAGCCCACACCTCACCAAGGGCCAGGAGCCACC**ATGTGGCGATGTCCACTGGGCTAC**
TGCTGTTGCTGCCGCTGGCTGCCACTTGGCTCTGGGTGCCAGCAGGGCTGTGGCGCCGG
GAGCTAGCACCAGGGCTGCACCTGCAGGGCATCCGGACGCCGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCCGGCCGTGCCAGCAGACTGTGCCCTGCCACTGGCGCCATCT
GTTACTGTGACCTCTCTGCAACCGCACGGCTCCGACTGCTGCCCTGACTCTGGGACTTC
TGCCTCGCGTGCACCCCTTCCCCGATCCAAGGATGTATGCATGGAGGCTGTATCTA
TCCAGTCTGGAAACGTACTGGACAACGTAACTGTAACCGTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGGCCCTCTGGGCATGACCTGG**TGAGGCATTGCTACGCCCTGGCACCA**
TCCGCCATCTCCTCGGTATGAAACATGCATGAAATTATACAGTGTGAACCCAGGGAG
GTGCTTCCCACAGCCTCGAGGCCTCTGAGAAGTGGCCAACCTGATTGAGCCTTGA
CCAAGGCAACTGTGCAAGGCCTCTGGCCTCTCCACAGCAGCTGTGGCATCCGATCGTCT
CAATCCATTCTCTGGGACACATGACGCCCTGTCCTGTCGCCAGAACCTGCTGTGAC
ACCCACAGCAGCAGGGCTGCCCGGTGGCGTCTCGATGGTGCCTGGTGGTCTCGCTG
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGCC
CTGCGCCCCCTGTATGATGCACAGCGAGCCATGGGTGGGCCAGGCCACTGCC
CACTGCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGG
AGAGGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCCCAACTCCTGGGCC
CAGCCTGGGGCGAGAGGGCCACTTCCGCATCGTGCAGGGCGTCAATGAGTGCACATCGAG
AGCTTCGTGCTGGCGTCTGGGCGTGGGAGGACATGGGTGTCATCACTGAGGCTG
CGGGCACCAAGCGGGGTCCGGCTGGGATCCAGGCTAACGGCCGGCGGAAGAGGCCCAATG
GGCGGTGACCCAGCCTCGCCGACAGAGCCGGCGCAGGCCGGCGCAGGGCGCTAAC
CCCGCGCGGGTCCGCTGACGCAAGCAGGCCCTGGAGCCGGCAGGGAGACTGGCG
GAGCCCCCAGACCTCCCAGTGGGACGGGGCAGGGCTGGCTGGGAAGAGCACAGCTGAG
ATCCCAGGCCTCGCGCCCCACTCAAGACTACCAAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCCACCCCAATCCGTATTCTTTTTTTTTAGACAGGGTCTGCTCCG
TTGCCAGGTTGAGTGCAGTGGCCATCAGGGCTCACTGTAACCTCCGACTCTGGGTCA
AGTGCACCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCAACACCTGGC
TAATTTTGTATTTTGAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTCAACT
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCCCTCCAAAGTGTGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTCACTGTTAAAAA
AAAAACCAAAAGTATTGATAAAAAAAA

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDC
ALPYLGAIICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEQRLLGHDPG
```

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCCTTTTCCACAGCAAGCTNTGCNATCCCGATTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCCTGCTCCTTNGCCCCAGAACCTGCTGTCTTGTCACACCAC
CAGCAGCAGGGCTGCCGCGNTGGCGTCTCGATGGTGCCTGGTGGTTCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGCGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCCATACAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATAACGCCGGCATGGACCCACTCAG

FIGURE 8

GCTGCTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGATGACTGCCTGCAGGTGGAGAATGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCATCCGCGAGTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTGGGGACCCGGCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGTGGGACGTCCTGCTGGTCCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCCTGACCCCTGGCCCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCAACCCCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCTTAACCCCTGTGCTCAGGCACCTCTTCCCCAGGAAGCCTT
CCCTGCCACCCATTGACTTGAGCCAGGTCTGGTCCGTGGTCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCAGTAAAGGCTGAGATGAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGCCTGGAGGCTGGGAGGAA
GGGGCCAGGCCTCACATTCGTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAAA

FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSLDT
DPPADGPSNPLCCCFHGPAFSTLNPLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCCACCGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCGCCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACTCAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCGGAGATCCCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTCACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGAAGAGCAAAGACTG
CGTGTTCACGGAGATCGTGCAGGAGAACAACTATAACGGCCTCCAGAACGCCGGCACGAGG
GCTGGTTCATGGCCTTCACGCCAGGGCGGCCAGGCTCCCGCAGCCGCCAGAAC
CAGCGCGAGGCCACTTCATCAAGCGCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC
CGAGAACAGAACAGCTCGAGTTGTGGCTCCGCCAACCGCCGGACCAAGCGCACAC
GGCGGCCAGCCCTCACGTAGTCTGGGAGGCAGGGGCAGCAGCCCTGGCCGCCTCCC
CACCCCTTCCCTTAATCCAAGGACTGGGCTGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCTGAGGCCCGAAGCATCCGAGCCCCCAGCTGGGAAGGGCAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTGCCCTTCCCGACGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTCAACCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCCTGAAGCC
CGCTGAAAGGTAGCGACTGAAGGCCTGCAGACAACCGTCTGGAGGTGGCTGCCTCAAAA
TCTGCTCTCGGATCTCCCTCAGTCTGCCAACCTCCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTCAAGGAAAAAGAAAGGGAGAGAGAGGAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCACTCCAGCCC
CGGAATAAAACCATTTCCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRKGKLIGKPSGKS KDCVFT EIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAATTCTCCCTGTTGAATTTCGCACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTAGCTGGAGTCTGGACTCAACAGAACCCATCCAGT
CATTGGATTTGCTGTTATTTTTCTTTTCTTTCCCACACATTGTATTTAT
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGCTTTTCT
GAAGTCTGGCTTATCATTCCCTGGGGCTACTCACAGGTGTCCAACACTCTGGCCTGCC
CTAGTGTGTGCCGCTGCGACAGGAACCTTGCTACTGTAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACAAATTATAATGC
TGGATTCCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTCCAAGAACATGTCAAGAGTTCTCCATTGCAAGGAAAAC
AATATTCAAGACCATTTCACGGGCTGCTCTGGCCAGCTCTGAAGCTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGTGAAGACGGGCCTCCGGAGGCTATTAGCC
TCAAATTGTTGTTTGTCTAAGAACATCACCTGAGCAGTGTGCCTGTTGGCTTCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCGACATGGCCTTCCAGAA
TCTCACGAGCTGGAGCGTCTTATTGTGGACGGAACCTCCTGACCAACAAGGGTATGCCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTACGTAATTGCTGTCC
CACCCCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACCAGAT
AAACACATTCTTGCACAGCCTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGTTTTGATAATCTCCAACCTGAAGCAGCTC
ACTGCTCGGAATAACCCTTGGTTTGTGACTGCAGTATTAAATGGGTACAGAACGGCTCAA
ATATATCCCTCATCTCTCAACGTGCGGGTTTGTGCAAGGTCTGAACAAGTCCGGG
GGATGGCGTCAGGGAATTAAATGAAATCTTGTCTGTCCCACGACCCCCGGCCTG
CCTCTTCAACCCAGCCCCAAGTACAGCTCTCCGACCACTCAGCCTCCCACCCCTCTAT
CTCAAACCCTAGCAGAAGCTACACCCCTCCAACCTCTACCACATCGAACACTCCCACGATT
CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTCTGAACGGATCCAGCTCTATC
CATTTGTGAATGATACTTCAAGTCAGCTGGCTCTCTTCAACGTGATGGCATA
CAAACTCACATGGGTGAAAATGGGCACAGTTAGTAGGGGGCATCGTCAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
TGTAGTGCACGGATGCTTTAACTACCGCGCGTAGAAGACACCATTGTTAGAGGC
CACCACCCATGCCTCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGCTTGATGGGGCGCGGTGATATT
GTGCTGGTGGTCTGCTAGCGTCTTGTGGCATATGCACAAAAGGGCGCTACACCTC
CCAGAAGTGGAAATAACCGGGCGGCGAAGATGATTATTGCGAGGCAGGCACCAAGA
AGGACAACCTCCATCCTGGAGATGACAGAAACCAAGTTTCAGATCGTCTCCTAAATAACGAT
CAACTCCTTAAAGGAGATTTCAGACTGCAGCCATTACACCCAAATGGGGCATTAATT
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTCCAGACCTGGAGC
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCAGAACATTAGACTCTTGAGAA
CACACTCGTGTGTCACATAAGACACGCAGATTACATTGATAATGTTACACAGATGCAT
TTGTCATTTGAATACTCTGTAATTATAACGGTGTACTATATAATGGGATTAAAAAGTG
CTATCTTCTATTCAAGTTAACAAACAGTTGTAACCTTGTCTTTAAATCTT

FIGURE 13

MGLQTTKWPShGAFFLKSLLIISLGLYSQVSLLACPSVCRCRNFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPaelHNvQSVHTVLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQLLKLEELHLDNSISTVGVEDGAFREAIISLKLFLSKNHLSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNNLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMARVELNMNLLSCPTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTSKLPTIPDWDRERVTTPPISERIQLSIHFVND
TSIQVSWLSLFTVMAYKLTwVKMGSLSVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNRYRAVEDTICSEATTHASYLNNGNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLLVL
LSVFCWHMHKKGRYTSQWKYNRGRKDDYCEAGTKKDNLILEMTETSFQIVSLNNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGGAGCAAGCGCGCGGGAGACAGAGGCAGAGGCAGAAGCTGGGCTCCGTCTGCCCTCCCACGAGCG
ATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCAGAGGCCAGGAGAACCCGGGTGGCTCGGCCCTGCC
TCGCTTCCAGGCGCCGGCTGCAGCCTTGCCCCCTTGCTCGCCTGAAAATGGAAAGATGCTCGCAGGCT
GCTTTCTGCTGATCCTCGGACAGATCGTCTCCCTCCCTGCCAGGGCCAGGGAGCGGTACGTGGAGGTCCATCT
CTAGGGCCAGACACGGCTCGGACACCACCCCGAGACGGCCCTCTGGAGAGTCTCTGTGAGAACACAAGCGGGCAGACC
TGGTTTCATCATTGACAGCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGGACA
TCTTGCAATTCTTGACATTGGCTCTGATGTCAACCCAGTGGACTGGGCTGCTCCAATATGGCAGCACTGTCAAGAATG
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCGCTGCTCAAGAGGATGCGGCATCTGTCCACGG
GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAAACATCCGATTCTCGAAGACAGAGGGGGCCGGCCCTGA
GGGAGAATGTGCCACGGGTCTATAATGATCGTACAGAGTGGGAGACCTCAGGACTCCGTGGCCAGGGTGGCTGCTA
AGGCACGGGACACGGGCATCCTAATCTTGCCATTGGTGTGGGGCAGGTAGACTTCAACACCTTGAAGTCCATTG
GGAGTGGCCCCATGAGGACCATGTCCTCTGTGGCCAATTTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGACGGCCACATGTGCAAGCAGCACATTCTGCAACATCCCTG
GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAAGATCCAGGATCTGT
GTGCCATGGAGGACCAACTGTGAGCAGCTGTGTGAATGTGCCGGCTCCTCGTCTGCCAGTGCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGGCTGTGGACTACTGTGCTCAGAAAACCACGGATGTGAAAC
ATGAGTGTGAAATGCTGATGGCTCCTACCTTGCCAGTGCATGAAGGATTGCTCTAACCCAGATGAAAAAA
CGTGCACAAGGATCAACTACTGTGCACTGAAACAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGAAAACCTGCAGCCAGTGGACCACTGTGCAAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTGAACACGGAGATTCTTCGCTGCCAGTGCTCAGAAGGCTTCC
TCATCAACGAGGACCTCAAGACCTGCTCCGGGTGGATTACTGCCTGCTGAGTGACCATGGTTGTGAATACTCCT
GTGTCACATGGACAGATCCTTGCCCTGTCAGTGTCTGAGGGACACGTGCTCCGAGCGATGGGAAGACGTGTG
CAAATGGACTCTTGTGCTTGGGGACACGGTTGTGAACATTCTGTGTAAGCAGTGAAGATTGTTGTG
GCCAGTGTGTTGAAGGTTATATACTCCGTGAAGATGGAAAACCTGCAGAAGGAAAGATGTCTGCCAGTATAG
ACCATGGCTGTGAACACATTGTGTAACAGTGCACGACTCATACACGTGCGAGTGCTGGAGGGATTCCGGCTCG
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAAATCAACCCACATGGCTGCGAACACATTGTGTTA
ATAATGGGAAATTCTACATCTGCAAATGCTCAGAGGGATTGTTCTAGCTGAGGGACGGAGACGGTGAAGAAAT
GCACTGAAGGCCAACATGACCTGGCTTGTGATCGATGGATCCAAGAGTCTGGAGGAAGAGAATTGGAGGTG
TGAAGCAGTTGTCACTGGAATTATAGATTCTTGACAAATTCCCCAACGGCGCTCGAGTGGGCTGCTCCAGT
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTTCAACTCAGCAAAGACATGAAAAAAGCCGTGGCCC
ACATGAAAATCATGGGAAAGGGCTTATGACTGGCTGGCCCTGAAACACATGTTGAGAGAAGTTTACCCAAAG
GAGAAGGGGCCAGGCCCTTCCACAAGGGTGCCAGAGCAGCAGCATTGTTGACCGAGGGCTCAGGATG
ACGTCTCCGAGTGGGCCAGTAAAGCCAAGGCAATGGTATCACTATGTATGCTGTTGGGTTAGGAAAAGCCATTG
AGGAGGAACATACAAGAGATTGCTCTGAGGCCACAAACAAGCATCTCTCTATGCCGAAGACTTCAGCACAATGG
ATGAGATAAGTAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGGAACTGCCAAAACGGTCAACAGCAACAGAAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT
CCTGTTCTAATTTGCACTGCAACACAGATATCTGTTGAAGAAGACAATCTTACGGTCTACACAAAAGCTT
CCCATTCAACAAACCTTCAGGAAGGCCCTTGGAGAAAACACGATCAATGCAAATGTGAAAACCTTATAATGT
TCCAGAACCTTGCAAACGAAGAGTAAGAAAATTAAACACAGCGTTAGAAGAAATGACACAGAGAATGGAAGCCC
TGGAAAATGCCCTGAGATACAGATGAAGATTAGAAATCGCAGACACATTGTTAGTCATTGTATCACGGATTACAAT
GAACGCAGTGCAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAAACAATCAGTACTGA
GAAACCTGGTTGCCAGAGAACAAAGACAAGAAGTACACTAACTTGTATAAATTATCTAGGAAAAAAATCCT
TCAGAATTCTAAGATGAATTACCAAGGTGAGAATGAATAGCTATGCAAGGTATTGTTAATATACTGTGGACAC
AACTTGCTCTGCCCTCATCCTGCCATTGCAATCTCATTGACTATACGATAAAGTTGCACAGTCTTACTT
CTGTAGAACACTGGCATAGGAAATGCTGTTTTGTACTGGACTTACCTTGATATATGTATATGGATGTATG
CATAAAATCATAGGACATATGTACTTGGAACAAGTGGATTAAATACAATATTAAAATTCAACCTTCAG

FIGURE 15

MEKMLAGCFLILGQIVILLPAEARERSRGRSISRGRHARTHPOQTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFRKSEVERAV
KMRHLSTGTMGLAIQYALNIAFSEAEGARPLRENPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIQVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNPVGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKGPC
EHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTCRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDBGTCAKLDSCALGDHGCE
HSCVSSEDHFVCQCPEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLA
EDGKRCRRKDVKSTHGCEHICVNNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIDSILTISPKAARVGLLQYSTQVHTEFTLRFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFRSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKIAEEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEALESDGRQDS
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL
EEKHDQCKCENLIMFQNLANEERKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTAGCGGCTGGCTCCCGCGCACGCTCCGGCCGTGCAGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCAGGGCTGGCGCCCTGACTCCGTCCGGCCAGGGAGGGC
CATGATTTCCCTCCGGGGCCCTGGTGACCAACTTGCTGCGTTTTGTTCTGGGCTGA
GTGCCCTCGCGCCCCCTCGGGGCCAGCTGCAACTGCACTGCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGAAAGTGGTGTCTCCAGCGTGGTACACCTTGCACGGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGTCACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCCGAACCTGCTCCCTGGGCTGGAGGGCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTAATGGTTCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT
GTGGGGCAAACGTGACCCCTGAGCTGCCAGTCTCAAGGAGTAAGCCCCTGTCCAATACCA
GTGGGATCGGCAGCTCCATCCTCCAGACTTCTTGACCAGCATTAGATGTCATCCGTG
GGTCTTAAGCCTCACCAACCTTCGTCTTCCATGGCTGGAGTCTATGTCAGGCCAC
AATGAGGTGGGACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGTACCTGGTGGACTGGGGTGTGGCTGGCTGGTCC
CTTGTACCAACGCCGGGGCAAGGCCCTGGAGGAGCCAGCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGACCCCTGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCC
TTCCTCTGTACCTCCGACGCCCTCCGGCCACCCATGGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTAT**GATGAC**
CCCACCACTCATGGCTAAAGGATTGGGCTCTCCTCTATAAGGGTCACCTCTAGCAC
AGAGGCCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCAACCTCTC
TTTACTGTGGAAAACCCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTCCAGTCAGTGCAGCTCCAGGC
CCCCTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGGCAGAGGATAGGAAATCTC
TTATTAAAACATGAAATATGTGTTTTCAATTGCAAATTAAATAAGATAACATAA
TGTGGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRIQGVPHVGANVTLSQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTACQCNVTLEVSTGPGAA
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKAEDAIAPRTLWPKSSDTISKNGTL
SSVTSARALRPPHGPPRGALTPTPSLSSQALPSPRLPTTDGAHPQPISPPIPGGVSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCAC TGGGCCAC CGCCA **A**TGAAACGCCTCCGCTCTAGTGGTTTTCCACTTG
TTGAATTGTCCTATACTCAAAATTGCACCAAGACACCTGTCTCCAAATGCAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGGAATTAACTCAGTCCTGTGGCGAAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTCAGATCCAGCAGTAACCA
AGACAGGTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAAC TGCCATT
TAGATAATGTCTGTATAGCTGCAAATATTAAATAAAAACCTTAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATATAGAAATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAAACA
CTATCTCAGCCAAGGACACCCCTTCTAACTCAACTCTTACTGAATTGTAAAACCGGTGAAT
AATTTGTTCAAAGGGATACATTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAACTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTGATAACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTGAT
TCATATAACATGAAACATATTCACTCCTCATATGAATATGGATGGAGACTACATAAATATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATA
AGAGTATTGGTCCTTGCTTCATCATCTGACAACCTTTATTGAAACCTCAAATTATGAT
AATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCC
ACCCACATTATATGAAC TTGAAAAATAACATTACATTAAAGTCATCGAAAGGTACAGATA
GGTATAGGAGTCTATGTGCATTTGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTGCAATTGATGTCCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATT
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATT
ACCTTCTGGTCTTCAGTGAATTCAAAGCACCAGGACAACAATTCAAACAAATCTTGCTG
TAGCCTATTCTTGCTGAACTGTTCTGTGGGATCAATACAAATACTAATAAGCTCT
TCTGTTCAATCATTGCCGACTGCTACACTACTTCTTTAGCTGCTTTGCATGGATGTG
ATTGAAGGCATACATCTCATCTATTGTTGGGTGTCATCTACAACAAGGGATTTGCA
CAAGAATTTTATATCTTGGCTATCTAAGCCAGCCGTGGTAGTTGGATTTGGCAGCAC
TAGGATACAGATATTATGGCACAAACCAAGTATGTTGGCTTAGCACCCAAAACAAC
TGGAGTTTATAGGACCAGCATGCTAATCATTGTTAATCTTGGCTTGGAGTCAT
CATATACAAGTTTCGTCACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTGAGAAC
TAAGGTCTTGTGCAAGAGGAGCCCTCGCTCTGTGTTCTCGGCACCACCTGGATCTT
GGGTTCTCATGTTGTGACGCATCAGTGGTACAGCTTACACTTACAGTCAGCAATGC
TTTCCAGGGGATGTTCATTTTATTCCCTGTGTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTTCAAAATGTCCTGTTGGATGTTAAGGTAACATAGAGAAC
GTGGATAATTACAAC TGCAACAAATAAAATTCCAAGCTGTGGATGACCAATGTATAAAA
TGACTCATCAAATTATCCAATTATAACTACTAGACAAAAGTATTTAAATCAGTTTCT
GTTTATGCTATAGGAACTGTAGATAATAAGTAAAATTATGTATCATATAGATATACTATGT
TTTCTATGTGAAATAGTCTGTCAAAATAGTATTGAGATATTGGAAAGTAATTGGTT
CTCAGGAGTGATACACTGCACCCAGGAAAGATTCTTCTAACACAGAGAAGTATATGAA
TGTCTGAAGGAAACCAGTGGCTGATATTCTGTGACTCGTGTGCTTGAAACTAGTCC
CCTACCACTCGGTAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAACAGGGCAGA
ATATCAAACAGTGAAAAGGAATGATAAGATGTATTGAGATGAACCTGTTCTGTAGAC
TAGCTGAGAAATTGTTGACATAAAATAGAAGAACACATTACCAATTGCTTGTGAA
TTGTTCTGAACCTAAATGTCCACTAAACACTAGACTCTGTGTTGCTAAATCTGTTCTT
TTCTAATATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLVVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSNQDRFITNDGTVCIENVNANCHLDNVCIAA
NINKTLTKIRSIKEPVALLQEYVNRNSVTDLSPTDIITYIEILAESSSLGYKNNTISAKDTL
SNSTLTERFVKTVNNFVQRDTFVWWDKLSVNRRTHLTLMHTVEQATLRISQSFQKTTEFDT
NSTDIALKVFFFDSYNMKHIHPHMNMMDGDYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLKQPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF
WNYS PDTMNGWSSEGCELTYSNETHTSCRNCNLTHFAILMSSGPSIGIKDYNILTRITQLG
IIISLICLAI CIFTWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFC SIIAGL
LHYFFLAFAFWMCIEGIHYLIIVGVYIYNGFLHKNFYIFGYLSPAVVVGFSAA LGYRYYGT
TKVCWLSTENNF IWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVLVHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,

648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTCTTATTGAAACCTCAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAAATAACATTTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAATACTCACCTGATACCAGAATGGCAGCTGGTCTCAGAG
GGCTGTGAGCTGACACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCTCTGGCCTTCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGC CGGTGGGAGGAGTTCCCCGAAACCCGGCCG
CTAACCGAGGCCTCCTCCCGAGATCCGAACGGCCTGGGCGGGTCAACCCGGCTGGGA
CAAGAAGCCGCCCTGCCCTGCCCGGGCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGC
GGTGTGAGTGGGTGTGCGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGG
TGTCTGGCACCTACCGTGGGCCGTAAGCGCTACTATATAAGGCTGCCGGCCGGAG
CCGCCGCCGTCAGAGCAGGAGCGCTGCCTCAGGATCTAGGGCACGACCATCCAACCC
GGCACTCACAGCCCCGCAGCGCATCCGGCGCCAGCCTCCGCACCCCCATGCCGG
AGCTGCCAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCTCTGGCTGGCGTGGCCGGCGCCCCCTCGCCTCTCGGACGCCGG
CCACGTGCACTACGGCTGGGCACCCCCATCCGCCTGCCGACCTGTACACCTCCGGCCCC
ACGGGCTCTCCAGCTGCTTCCGTGCATCCGTGCCGACGGCGTGTGACTGCCGCCGG
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTCTGCCGACGGCAAGATGCAGGG
CGTGCACAGCGTGCCTGACCTCTGCATGGCGCCGACGGCAAGATGCAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTCGAGGAGGAGATCCGCCAGATGGTACAATGTGTACCGA
TCCGAGAAGCACCGCCTCCGGTCTCCCTGAGCAGTCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTCTTCCACTCTCATTTCTGCCATGCTGCCATGGTCCCAGAGGACCC
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG
GACCCATTGGCTTGTCAACGGACTGGAGGCCGTGAGGAGTCCCAGCTTGAGAAGTA
GAGACCATGCCGGGCTCTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGACG
TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTAGCTTAGGAAGAACATCTAGAA
GTTGTACATATTCAAGAGTTTCCATTGGCAGTGCCAGTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCCTGGGCCCCATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGCTCAGTTCTGCTGAATACTCCATCGATGGGAAC
TCACCTCCTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTCATCCTCACTTC
CCCAGGAGCAGCCAGAACAGCAGGCACTGTTAATTCAAGGAAACAGGTGATCCACTCTGA
AAACAGCAGGTAATTCACTCAACCCATGTGGAAATTGATCTATATCTACTTCCAGGG
ACCATTGCCCTCCAAATCCCTCCAGGCCAGAACACTGACTGGAGCAGGCATGGCCACCC
GCTTCAGGAGTAGGGGAAGCCTGGAGGCCACTCCAGGCCCTGGACAACTTGAGAATT
CTGAGGCCAGTCTGTCAATGGATGCTGCTGAGAATAACTTGCTGCTCCGGTGTACCTGC
TTCCATCTCCCAGCCACCAGCCCTGCCACCTCACATGCCTCCCCATGGATTGGGCCT
CCCAGGCCCCCACCCTATGTCAACCTGCACTTCTGTTAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTGTCAATAACTTGCTGTTGGAAGCAGCAGGGGGAGACCTAGAAC
CCTTCCCCAGCACTGGTTTCCAACATGATATTATGAGTAATTATTGATATGTACA
TCTCTTATTCTTACATTATTTATGCCCAAATTATTTATGTATGTAAGTGAGGTTG
TTTGATATTAAATGGAGTTGTTGT

FIGURE 22

MRS GCVVHV WILAGLWL AVAGRPLA FSDAGPHVHYGWGDPI RLHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLL EIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVS LSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETD SMDPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTGACCTCCTCA
GAGCAGCCGGCTGCCGCCGGGAAGATGGCGAGGAGGAGGCCACCGCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTCTGCCCAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGAAAACCCAA
AGAAGACTGTTCCAGATTAGAGTGGAAAGAAACTGGGTGGAGTGTCTCCTTGTCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAATGTGACAAGAAGTGATGCCGGAAATATCGTTGTGAAGTTAGTGCCCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATACTGCAACTCTGGAAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGAAATCCAGCTCCTGAATAACACATGGTTAAGGATGGCATCCGTTGCTAGAAA
ATCCCAGACTGGCTCCCAAAGCACCAACAGCTCATACACAATGAATAACAAAACGGAACT
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAAATTCCCTGTGAAGGCCGCAATT
TGGTGGATATCGCAGGTGTCCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTAGTGATTTCCGTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTGGAAATGTGCAGTGGCTCACGCCGTAACTCCAGCACTTGGAGG
CCGCCGGCGGGCGGATCACGAGGTCAAGGAGTTCTAGACCAGTCTGCCAATATGGTAAACCC
CATCTCTACTAAAATACAAAATTAGCTGGGATGGTGGCATGTGCCGTGAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTGAACCCGGAGGCAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAATAAAATAATA
AATAAAATACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

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FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKT
VSSRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVS
APSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDGEGNPAPEYT
WFKDGIPLLNPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN
SVGYRRCPGKRMQVDDLNISGIIIAAVVVA
LVIISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPAL
WKAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGCTAGCACTGAAACTGTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATTTAACATGCTCCACAGCCGGACCCTGGCAT
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGATTAAATATTTACTTCTAAATAA
ATGAATTACTCAATCTCTATGACCATCTACATACACTCCACCTCAAAAAGTACATCAATA
TTATATCATTAGGAAATAGTAACCTCTCTCCAATATGCATGACATTGGACAATG
CAATTGTGGACTGGACTTATTCAGTGAAGAAAACCTTGTGGTCTATGGCATTCA
TTTGACAAATGCAAGCATCTCCCTATCAATCAGCTCTATTGAACCTACTAGCACTGACTG
TGGAACTCTTAAGGGCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCTATGTGCTACTTGGCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACTTTCCCAGCCAGATTGCC
AGCTAACACACAGATTCTCTCCTACAGACTAACAAATATTGCAAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTACTGGCCTGGATTATCTCAAAACAATTATCTCAGTCACCAAT
ATTAATGTAAGGAAAGATGCCTCAGCTCCTTCTGTGTACTAGAGGAAAACAAACTTACTGA
ACTGCCTGAAAATGCTGCGAAGTGGCAACTTACAAGAACTCTATATTAAATCACAAC
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTCTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTCCAAATCTAGAGAT
TCTGATGATTGGGAAAATCCAATTATCAGAACATCAAAGACATGAACATTAAAGCCTTATCA
ATCTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACAGATAACGCCTGGTT
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTAAAGTACCCATGT
TGCTCTCAAAAGTGTAAATCTCAAATTGGATCTAAATAAAACCTTATTAAAG
TACGAAGGGGTGATTTAGCAATATGCTACACTAAAAGAGTTGGGATAAATAATATGCCT
GAGCTGATTCCATCGATAGTCTGCTGTGGATAACCTGCCAGATTAAAGAAAATAGAAGC
TACTAACACCCCTAGATTGTCTACATTCAACCCCAATGCATTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCAGTGCCCTGTACCATGGTACCTGGCTCT
CCAAACCTCAAGGAATCAGCATACACAGTAACCCATCAGGTGTACTGTGATCCGTTG
GATGAACATGAACAAAACCAACATTGATTGATGGAGCCAGATTCACTGTTGCGTGGACC
CACCTGAATTCCAAGGTCAAAGTGTGAGAGCTTCTTCTAAATCTAAATGTAGAAGCTGGAGCTATGT
CTCCCTCTTATAGCTCCTGAGAGCTTCTTCTAAATCTAAATGTAGAAGCTGGAGCTATGT
TTCCTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTCTG
GTCAAAAACCTTGCCTAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAAACACTA
GATATAATGGCGTAACTCCCAAAGAAGGGGTTTATATACTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAATG
GCTCTTGAATATTAAAATAAGAGATATTCAAGGCCAATTCACTGTTGGTGTCTGGAAAGCA
AGTTCTAAATCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATCTCA
TGCTGCGCAAAGTGTGCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTACAGAAAACAGAAAAAAA
TGTGTAAATGTCACCACCAAGGTTGCACCCCTGATCAAAAAGAGTATGAAAAGAATAATAC
CACAAACACTTATGGCTGTCTGGAGGCCCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCCAGAAATGAACGTGTGATGGTGACACAGCTATGTGAGGAATTACTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGATAAAATCTCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTATAGGTTACCAACAAATATGTCCT
AAAAACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNAKIEYSTDGPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELSNLQELYINHNLSTISPGAFIGLHNLLRLHLNSNRQLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSVIAGINLTEIPDNAVGLENLESISFYDNRL
IKVPHVALQKVVLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSALVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHTIESLPNLKEISIHSPNIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQNRQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLLGIIGVICLISCLSPEMNC DGGHSYVRNYLQKPTFALGELYPP LIN
LWEAGKEKSTSLKVKA TVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCAGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTATTATGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTGTTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTGTTCCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAATGCCTCAATAACCTGAAGGCCAGGCCAGAATTGCCAACAAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTGGCTGGTTCACTATGGTGTCTCATATGTGGTATATTATGTGAGGAAAATCAGGAG
GATGCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATGTGTCCAAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTGCGATTGCAGTAGAAATAAGTGGTTACTTCTCCCATCCATTGTAAACACATTGAA
ACTTTGTATTCAGTTTTTGAAATTATGCCACTGCTGAACTTAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAATAATGAAATTATTTTTT
AATTAAAAGCAAATAAAAGCTTAACTTGAACCATTGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLQSFVLMILCFHSASMC PKGCLCSSSGGLNVTC SNANLKEIPRDL
PPETVLLYLD SNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNICKTSVLDEHAGR PFL
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCAGCAGGATTGCAGGTGAGCAAGAGGAATGCTGGCGGG
GGCGTGAGGAGCATGCCAGCCCCCTCTGGCCTGCTGGCAGCCCACCTCCTGCTGGTGT
GGGCTCAGTGTGTCAGGCTGGCCACGGGCTGCCGCCCCGCTGCGAGTGTCCGCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGTGTTGAGCTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATAAAACGCTCAACCAGGACGAGTTGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGGAGGCCG
CCTTAACAAACCTCTAACCTCCGGACGCTGGGTCTCCGAGCAACGCCCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCCTCAGAACCTGACCAAGCAGGACATCAGCGAGAACAGAT
CGTTATCCTACTGGACTACATGTTAGGACCTGACACCTCAAGTCAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCACCGCGCTTCAGCGGCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGGCTGTCCCACCTGCACGGCCT
CATCGTCCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTTAAGAGGC
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCCTACTGGACACCATGACACCCAAC
TGCCTCTACGCCCTAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCCGCCACCTAGTCTATCTCGCTTCAACCTCCTACAACCCATCA
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGC
GGGCAGCTGGCGTGGTGGAGCCCTATGCCCTCCGGCCCTCAACTACCTGCGCGTGTCAA
TGTCTCTGGCAACCAGCTGACCAACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG
AGACACTCATCTGGACTCCAACCCGCTGGCCTGCGACTGTCGGCTCCTGTGGTGTCCGG
CGCCGCTGGGGCTCAACTCAACCGCAGCAGCCCACGTGCCACGCCAGTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCAACTACTCACCGCCCG
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTGTGGACGGGCCACACGGTGCAGTT
GTGTGCCGGGCGATGGCAGCCGCCATCCTCTGGCTCTCACCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCCGGCAACGAC
TCCATGCCGCCACCTGCATGTGCGCAGCTACTGCCGACTGGCCCCATGCCAACAA
GACCTCGCTTCATCTCAACCAACGCCGGGAGGGAGAGGCCAACAGCACCGCGCACTG
TGCCTTCCCCCTCGACATCAAGACCTCATCATGCCACCACTGGCTCATCTCTTTC
CTGGCGTGCCTCTCTGCCCTGGTGTGCTGTTCTCTGGAGGCCGGCAAGGGCAACAC
AAAGACAACATCGAGATCGAGTATGTGCCCCAAAGTCGGACGCAGGCATCAGCTCCGCC
ACGCCGCCGCAAGTTAACATGAAGATGATATGAGGCCGGGGCAGGGACCCCCG
GGCGGCCGGGAGGGGAAGGGGCTGGTGCACCTGCTACTCTCAGTCCTCCACCTC
CTCCCTACCCCTCTACACACGTTCTCTTCTCCCTCCGCCCTCCGCCCCCTGCTGCCCG
CCAGCCCTACCCACCTGCCCTCTTCTACAGGACCTCAGAACGCCAGACCTGGGGACCCCA
CCTACACAGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTCA
ATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACTGGGTTCAATAATTATGGATT
TATGAAAATGAAATAATAAAAAAGAGAAAAAACTAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTL
GLRSNRKLIPLGVTGLSNLTQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVEISH
WPYLDLTMTPNCILYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMHL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVNVSGNQLTLEESVFHSVGNNLETLLDSNPLA
CDCRLLWVFRRRWRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVFPDGTLEVRYAQVQDNGTYL
CIAANAGGNDSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCACACGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGCGCCCTTCGGTCAAC
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGGATTCAAGGCTGCCAGGCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATGGGGCCCCAGCCGCTCGCTCCTGCTCCTGCTCCTGC
TGTCGCCTGCTGGCTGGCGCCGGCGGGCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGTCAAGTGCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGCTAACCTGCTCAGCAGACTCTCTACTTTGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCAAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCGTG
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCACTGGTT
ATAAAATCTTCAATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCAAGTCTCTGGGAGCAAG
CCTGCAGCCGGCTCACCTGGAGAAAGGGTACCAAGAACACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCAAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCAGATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCCGGAATCCAGTCC
CCCAGCAGTACCTATGGGAGAACGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTCCCTTCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCA
CAACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCGGTGCCT
CCTCCTCCAGCACCTACCACGCCATCATCGTGGATCGTGGCTTCATTGTCTCCTGCTG
CTCATCATGCTCATCTCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAGGCTCCGACGATGCTCCAGACGCCAACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTCATAGAGGCGCCTGCCACTTCTGC
GCCCCAGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCCGCTGCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTGACTCGGTTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTGTAAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGGCCCTGGGTGAGAAAAGCAAAAAACA
AACAAAAAACA

FIGURE 32

MGAPAASLLLLLFFACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSIISNVALADEGEYTC SIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTCTTCCTTCTGG
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTAAAAATGCCTGCTTGATTCTGTT
GCTGGAGACGTCTTTGCCGCTGGAACGTTACAGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTTCCAGTTACCATTATTCTGCATGGCAATT
CCTCACTCGACTTTCCCTAATGAGTCGCTAACCTTATAATGCGGTTAGTTGCACATGG
AAAACAATGGCTTGCATGAAATCGTCCGGGGCTTTCTGGGGCTGCAGCTGGTAAAAGG
CTGCACATCAACAACAAGATCAAGTCTTTCGAAAGCAGACTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC
GTGTTCCAGTATGTGCCCATACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCC
GGGACTGCACCTGTGATCTGCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGCCAGTGGCTCGGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGTCCTTGAAAAAACGAGTGGATTCTAGTCTCCGGCGCCCC
CCCAAGAACAGGACCTTGCTCCCTGGACCCCTGCCAACCTCCAGGGTGGTTAAAGATGAAC
GATCATGCCAACACCAGGGTCTGCTCAAACGGAGGTACAAAGATCCCAGGAACTGGCAGAT
CAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAAC
GTTTACCTGCCCTGGGGCTGCAGCTGCGACCACATCCCAGGGTGGTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTGGCTGATTGAAGGCCAACGCTCTAACGTGCAGGA
GCTTTCCCTACGAGATAACAAGATCCACAGCATCGAAAATCGACTTGTGGATTACAAGA
ACCTCATTCTGGATCTGGCAACAAATAACATCGCTACTGTAGAGAACAAACACTTCAAG
AACCTTTGGACCTCAGGTGGCTACATGGATAGCAATTACCTGGACACGCTGTCCGGGA
GAAATTCGCGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCGGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTAACAAACACTG
CTGAGGTCCCTGCCTGGACGTGTCGCTGGGGCTCGCTCTAAACTCAGCCTGCACAA
CAATTACTCATGTACCTCCGGTGGCAGGGTGGACCAAGTTAACCTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGAGTGCTCCTGCACAATTGTGCCCTTAAGCAGTGGCA
GAACGCTTGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCT
TAGAAAGGATTTCATGCTCCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTAACTCGCACAGTAAAACAGCACTGGGTTGGCGAGACCGGGACGCACTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTGGTGTGGTCCGGACTGCTGCTGGT
GTTTGTACCTCCGCCTCACCGTGGCATGCTCGTGTATCCTGAGGAACCGAAAGC
GGTCCAAGAGAGCAGAGATGCCAACTCCTCCGCTCGAGATTAATTCCCTACAGACAGTCTG
GAECTTCTACTGGACAATGGCCTTACAACCGAGATGGGCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCAGACTAAAGACCCCAACCCAAATAGGGGAGGGCAGAGGGAAAGGCG
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGGCGTGTACCCAAATCCCC
CCATCAGCCTGGATGGCATAAGTAGATAAAACTGTGAGCTCGCACAAACGAAAGGGC
GACCCCTTACTTAGCTCCCTCCTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCTTTGCTGAGAGCCCCTTGACAGAAAGCCCAGCAGCACCCCTGCTGGAAG
AACTGACAGTGCCTCGCCCTCGGCCCCGGGCGTGGATGCGCGGTTCTATAC
ATATATAACATATCCACATCTATATAGAGAGATAGATATCTATTTCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAACTTGACTTCTGAC

FIGURE 34

MLLWILLLETSCLCFAAGNVTGVCCKEKCSCNEIEGDLHVDCEKKGFTSLQRFTA
PTSQFYHLFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPG AFLGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAFQDLNKLEVLI
LNDNLISTLPANVFQYVPITHLDLRG
NRLKTLPYEEVLEQI PGIAEILLEDPNWCDCTCDL
LSLKEWLENIPKNALIGRVVCEAPTRLQ
GKD
LN
ETTEQDLCPLKRN
VDSSL
PAPP
A
QE
ET
F
AP
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PL
PT
PF
KT
NG
QED
HAT
PG
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GT
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IPGN
WQ
IKIR
PTAA
IAT
GSS
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GL
KM
NC
NN
RN
V
SSL
AD
LK
P
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KLS
NV
QEL
FLR
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KSH
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C
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S
L
S
D

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCTGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGACACATTTCTGTGCGGGCTAAGGGAAACTGTTGGC
CGCTGGGCCCGGGGGATTCTTGGCAGTTGGGGGTCCGTCGGAGCGAGGGCGGAGGGG
AAGGGAGGGGAACCGGGTTGGGAAGGCCAGCTGTAGAGGGCGGTGACCCGCTCCAGACAC
AGCTCTGCGTCTCGAGCGGACAGATCCAAGTGGGAGCAGCTGCGTGCCTGGGGCCTCAG
AGAATGAGGCCGGCGTCTGCCCTGTGCCTCTGGCAGGCGCTCTGGCCCGGGCGGCGG
CGGCGAACACCCCACGTGCCGACCGTGTGGCTCGGCCCTCGGGGCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGGCCGAGGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCCCGAGCTGCGCCTGTGCTCGCCTCGGGCAGGCCAGG
GCCCGGAGGGGCTCAAAGACCTGCTGTTCTGGGTGCACTGGAGCGCAGGCCTTCCACT
GCACCCCTGGAGAACGAGCCTTGCGGGGTTCTCCTGGCTGTCCTCGACCCCGGGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGGGAGATGCGC
GGTACTCCAGGCCACCGGTGGGGTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGTACCTGTGCAAGTACCAAGTTGAGGTCTTGTGTCCTGCGCCGCCCCGGG
GCCGCCTCTAATTGAGCTATCGCGGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGCGCTCGCTGGACAAACTCTCGGGCATGTGTTGTGTCCTGCCCC
GGGAGGTACCTCGTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG
CTTGCCCTGGAATGTGCTACGGGCTTCGAGCTGGGAAGGACGGCGCTTTGTGACCA
GTGGGAAGGACAGCCGACCCCTGGGGGACCGGGTGCCTCAGGCGCCGCCGGCCACT
GCAACCAGCCCCGTGCCGAGAGAACATGCCAATCAGGGTCGACGAGAACGACTGGGAGAGAC
ACCACTTGTCCCTGAACAAGACAATTCACTAACATCTATTCTGAGATTCTCGATGGGAT
CACAGAGCACCGATGTCTACCCCTCAAATGTCCCTCAAGCCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGATTCCAAGTTAATTCTACGACTTCCTCTGCCACTCCTCAGGCTTT
CGACTCCTCCTCTGCCGTGGTCTTCATATTGTGAGCACAGCAGTAGTAGTGTGGTGTGATCT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCAGAAAGCCCCTTCCCAGCCA
AGGAAGGAGTCTATGGCCGCCGGCTGGAGAGTGATCCTGAGGCCGCTGTTGGGCTC
CAGTTCTGCACATTGCACAAACATGGGTGAAAGTGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCCTTGCTGGCGGAGTCCCCTTGGCTCTAGTGATGCAT**AGGAAACAGGGGA**
CATGGGCACTCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACCTAC
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCCTCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA
TGGTGATACTGGGGACCGGGTAGTGCTGGGAGAGATATTCTTATGTTATTGGAGAA
TTTGGAGAAGTGATTGAACCTTCAAGACATTGAAACAAATAGAACACAATATAATTACA
TTAAAAAAATAATTCTACCAAAATGAAAGGAAATGTTCTATGTTGTTCAGGCTAGGAGTAT
ATTGGTTGAAATCCCAGGGAAAAAAATAAAAATAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGL
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGFFACECATGFELGKDGRSCVTSGEQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILTMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGATT CAGCAGTGGCTGTGGCTGCCAGAGCAGCTCCTCAGGGAAACTAAG
CGTCGAGTCAGACGGCACCATATCGCCTTAAAAGTGCCTCCGCCGTGCCGGCGTATC
CCCCGGCTACCTGGGCCCGCCCGCGCGGTGCGCGCGTGAAGAGGGAGCGCGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGGTGTGAGCGCGGTGGGTGCGGA
GGGGCGTGTGCCCAGCGCCACTCTGCCTGCTGGCTGCCACCCAGCTCTCGCG
CAGCAGTCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCAAATAGCAAATGTA
CTGGAAAATCA
CAGTCCCAGAGAAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCATGCCAATGCCAGCGCATTGGCG
CTTCTGTGGCACTTCCGGCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGGCATGTTCTCCGCTGTAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTAAA
CCCCAACTGGCCAGACCGGATTACCTGCAGGAGTCACTTGTGTGGCACATTGTAGCCC
CAAAGAACATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGGGAAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGTAGTCCACCTGCAGCAATTGTGTCTGAGAGAAATGAACCTCTTATTCA
TTTATCAGACTTAAGTTAACAGATGGTTATTGGTCACTACATATTCAAGGCCAAA
AAACTGCCTACAACACAGAACAGCCTGTCACCACATCCCTGTAACCACGGTTAAA
ACCCACCGTGGCCTTGTCAACAAAAGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAACCATCACTCGCGATGGGAGTTG
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTGGCATTGAGCAGGG
CAAGAACATGAGTGCAGGCTGACTGTCGTCTGCAAGCAGTGCCTCTCAGAAGAGGTC
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGCAAATCATGCCAACAGC
TTTATCATGATGTTCAAGACCAAGAACATCAGAAGCTCCTGGATGCCTAAAAA
AAGCAATG
TTAACAGTGAACGTGTCATTAAAGCTGTATTCTGCCATTGCCATTGAAAGATCTATGTT
CTCTCAGTAGAAAAAAACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GA
CTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAAGTTCTT
TGCCTGCTGTCAGAGGAGCAGCTATGATTGGAAACCTGCCACTTAGTGCAGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAAGCGTTATTATACATCTGTAAAAGGAT
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAAGATTAGAAGTGCAATATTATAGT
GTTATTGTTCACCTCAAGCCTTGCCTGAGGTGTTACAATCTGTCTTGCCTTCTA
AATCAATGCTTAATAAAATTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESNDLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTITRD GSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

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CGGACGCGTGGCGGGACCGCGTGGCGGCCACGGCGCCGCGGGCTGGGCGGTCGCTTCTT
CCTTCTCCGTGCCCTACGAGGGTCCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTCAACCTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAACCATCCGGGACAACACTTGGAG
GTGGAAACACTGCCTGGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCCCGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGAAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAACGCCAGGCATCTGGTATGTCGGCTTGT
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGGCATCTGGTATGTCGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCA
ACTGTGGAGCTGACCAATTCTCGGTGAAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCCTAGGCTGCATGGGGCAGGGCCAGGTGCGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGAGAGA
ACAAGCAGTGTAAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGCTGCAGCAGATGTTCTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCAGTTGGTGTACCGCCATCTCATTGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTCAGAGCGCAGTGCAGCGTGTGGAGGGCTCATCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCCTCCACCCACGCTGCCCGAGAGCTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTGGTTATTTGAGAGTGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTCACCTGGGGGGACTGGCAGGCTCACAATGTGTGA
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCTGCCAGTTCTGT
TCTGTGTTCACCAACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAAGA
AAGGTCTTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPKGLVPAVLWGLSLFLNLPPIWLQPSPPPQQSSPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLESELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPGPGTERPCGGYGCCEGETRGGSGHCDCQAG
YGGEACGQCGLGYFEAERNASHLVCASFPCARCSGPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGMGAGPGRKKCSPGYQQVGSKCLDVDECE
TEVCPGENKCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAKGDLVFTAIFIGAVAAMTGYWLRSRDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCTCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGGCAGCTGCAGCTCAAAGAGGT
GCCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGGGAAAGAGGTTCAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTCAGGCCGTGCTGCCGTCTCCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGCGGCTGTCCCCGCGCAGCGCCGGGCC
CGGGTGACCGTCGAGTGGCTGCCGTCCACGAGAGGGCTGGAAGGCCCTCGACGTGACCGAGGCCGTGA
CTCCAGGCTGGTGTCCGTCCACGAGAGGGCTGGAAGGCCCTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGC
GCCAGCCGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGGCCAGAACACTGGTGGTGGAGCCCCCGGGCTT
CCTGGCTTATGAGTGTGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTTAAGTGGC
CGTTCTGGGCCTCGACAGTCATGCCCTGGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGGCCAAGGAGGCTCCAGCCATGGCGCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGGTCAAGGAGGTAACAGGAGAGCTG
GCGATGACTGAACTGCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTTGCTCTCAGGAATGAGAATCTTGCCACTGGA
GAGCCCTGCTCAGTTCTCTATTCTATTACTGCACTATATTCTAACGACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTGTCATTGTTACTGTGCTGTCAC
TGGATCTGGCTAAAGTCCTCCACCACACTCTGGACCTAACAGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTTGAAAACATGAATAAACACATTTTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAALTGEQLLGSLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEHQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCTQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

TOOT TOOT TOOT TOOT TOOT

GTCTGTTCCCAGGAGTCCTCGGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTTGTCCCTGTGCCTACTCGGGCTTTCTTCTCCCCGTGGAGTGGAAAGTTGACCA
AGGAGACACCAACCAGACTCGTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGATGGTCTCTGAGGAAGGCGAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAAAGATGGTCCCCACCTCTGAATACACACTGGTTCAAAGAT
GGGATAGTGTGCTACGAATCCAAAAGCACCCGTGCCTCAGCAACTCTTCCTATGTCCT
GAATCCCACAACAGGAGAGCTGGTCTTGATCCCTGTCAGCCTCTGATAACTGGAGAATACA
GCTGTGAGGCACGGAAATGGTATGGACACCCATGACTTCAAATGCTGTGCGATGGAAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCCTGATTCTCCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCGAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTCACCGCCTATCATCTGCATTGCTTACT
CAGGTGCTACCGGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCTTATTGTCTTC
TACACCCACAGGGCCCCCTACTTCTCGATGTGTTTAATAATGTCAGCTATGTGCC
ATCCTCCTTCATGCCCTCCCTCCCTTCTACCAACTGCTGAGTGGCCTGGAAACTTGTGTTAAA
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGAAAAATGGCGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTCTTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTGCTCTCCATGGGAAGTG
CCACTGGATCCCTGCCCCCTGAATACAAGCTGACTGACATTGACTGTGCTGT
GGAAAATGGGAGCTCTGTTGGAGAGCATAGTAAATTTCAGAGAACTTGAAGCCAAAAG
GATTAAAACCGCTGCTCTAAAGAAAAGAAAATGGAGGCTGGCGCAGTGGCTCACGCC
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGAGTTGGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCC
CTAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPKLSCAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEGFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCGCTGTGGGACAGCATGAGCGGCCGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGCTCTGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCCGAGCCGTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG
GCTCGTGCACCCCACCAAGTTCCAGTGCCGCACCAGTGGCTATGCGTGCCTCACCTGG
CGCTGCGACAGGGACTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA
GTGACTGCTTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCGACTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCCGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCACCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCCTCTGTCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCAACTGCCTATGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCCTCCTCCTTGTCCCTGGCTCCGAGGCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAACAGAC
CTCGCTGCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGTGCGGATGGTACCCGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACAG
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLDCCSDGSDEEECRIEPCTQKGQC PPPGLPCPCTGVSDCSGGTDKKL
RNC SRLA CLAGELRCTL SDDCIPLTWRCDGHPDCPDSSDEL GCGTNEILPEGDATTMGPV
LESVTSLRNATTMGPVTL E SVPSVGNATSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLG LLVAMKESLLLSEQKTS LP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCACCGCGTCCGGTCTCGCTCGCGCAGCGGCCAGCAGAGGTCGCGCACAGATGCGG
GTTAGACTGGGGGGGGAGGAGGAGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG
GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTGC
GCCGTGATCCTGTGGTTTAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTCAAGTGTGCTGACCCCGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTCTTGAAGGCTCTGTAGCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCCCTAGGCTGGATCCAAAGTGA
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA
ACAAGACATATAGACATGGAGAGAAGCTAACATCACTTGTATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCAATTGTGCGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTCCCGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTTAAACTT
GATGGGTCTGCGTATCTGAGTGCTTACAAACCTTATCTGGTGTCCAGGCCACCCGGTG
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCAAATGGTAGTCACGGAGATTCGTCT
GCCACCCGGCCTTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTACTGCGATCCT
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCCCTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGGTGTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCTCCCCGGAG
TTCCAGCAGTGACCCCTGACTTGTGGTAGACGGCGTGCCGTATGCTCCGTCTATG
ACGAAGCTGTGAGTGGCGCTTGTGAGTCCTAGGCCCCGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTGAGCTGCCAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCCGTTGGACAAACCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCAGGCATCCATCATGCCACTGGGT
GTTGTTCTAAGAAACTGATTGATTAAAAAATTCCAAAGTGTCTGAAGTGTCTCTCAA
ATACATGTTGATCTGTGGAGTTGATTCCCTTCTCTGGTTTAGACAAATGTAAACAA
AGCTCTGATCCTTAAAATTGCTATGCTGATAGAGTGGTAGGGCTGGAAGCTTGATCAAGTC
CTGTTCTTCTGACACAGACTGATTAAAATTAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGVFFEGSVARFHQCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPIQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASNDPDIIASTAEEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCACCGCGTCCGCTCCGCCCTCCCCCGCCTCCGTGC GGTCGGTGGCCTAGAGA
TGCTGCTGCCGGTTGCAGTTGTCGCACGCCCTGCCGCCAGCCCGCTCCACCGCCGT
AGCGCCCGAGTGTGGGGGGCGACCCGAGTCGGGCCATGAGGCCGGAACCGCGCTACAGG
CCGTGCTGCCGTGCTGGGTGGGCTGCCGCCAGGGTCGCCTGCTGAGTGCC
TCGGATTGGACCTCAGAGGAGGGCAGCAGTCTGCCGGGAGGGACACAGAGGCCTGTTA
TAAAGTCATTACTTCATGATACTTCTCGAAGACTGAACTTGAGGAAGCCAAGAACGCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTCATTGAAAACCTCTGCCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCCTGA
GGAGAAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATA
CACAAATTAGGAACGGTATGGATGAGCCGTCTGCCAGCGAGGTCTGGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACAAATTCTTGCAAATATTCTGATGAGAAACCAGCAGTCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTCCAGAAGAACACAG
GAAGAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAAGCTGCCCTGAATCTGGCTACAT
CCTAATCCCCAGCATTCCCTCTCCTCCTTGTGGTACCAAGTGTATGTTGGTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCTAGCACAAAGAACACACCATC
TGGCCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTCTTGAGTGTGTT
CGGGAGAAGCCACTCCGATGACATGTCTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACCAAATGGGAGGAGTAAGGAGTCTGGATGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAACTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAAATC
CTCTTATTTCTATAAGGAAAATACACAGAACGGTCTATGAACAAGCTTAGATCAGGTCTGT
GGATGAGCATGTGGTCCCCACGACCTCCTGGACCCCCACGTTGGCTGTATCCTTAT
CCCAGCCAGTCATCCAGCTGACCTTATGAGAACGGTACCTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCACTTGTTGGTGTATCTAACTTTAAGGGACAGAGCTTACCTG
GCAGTGATAAAAGATGGCTGTGGAGCTTGGAAAACCACCTCTGTTCTGCTATACAG
CAGCACATATTATCATAACAGACAGAAAATCCAGAACATCTTCAAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGCAATTCTCATATCTGTTTTCAAAGAACAAAATCAAATAAGA
GCAGGAAAAAA

TGGATGGCTGGCTGG

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGQLVSIESEDEQKLIEKFIENLLPSDGFDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKKTFKESREAALNAYILIPSIPLLLL
VTTVVVCWWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSESGFVTLSVESGFVTNDIYEFS
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

TOP 20% 30% 40% 50% 60%

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGTCCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCGCTGAGCCCCGGCGCCGCAGAAGACTTGT
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
GTTCAAGCATGCGCTTGTGGACCCCAGTGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTGTTGCTGACACGGGGCTGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC
AGTTGATTACACAGTCACCAATCTAGCTGGTGGCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
TTTCACCAACCTTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTAGAAGTCTTGTATCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCAGGCAGGCACACAAACCTCCAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCGGACAAGATCAGAAAGCTGTATCTCTATGCCGCTCATGATG
TGACCTTCATACCGCTTTAATGACCTGGGATTTTGACCAAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACCTTACAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACACGGGAAGGAGCAGGTGCCAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGT
TCTTGAAATGCCATGTCAGTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPGVVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFAALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAEQAHLNPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLIES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTAACATACTTGCAGCTAAACTAAATATTGCTGCTGGGACCTCCTCTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTGACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGCAACCGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGAACAGAACAGATACTGGCTCAGTGTGAGCAAGAACAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTTTCTCCCCA
GTCCCAGAGGGTGTCAAGGCTGGCTGACGCCCTGGCATTGCAAGGGACGCGTGGAAAGTGA
GCACCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCCAAAGGTGG
TGTGCCGGCAGCTGGATGTGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAACCCATCTGGCTGAGCCAGATGTCTGCTCAGGACGAGAACGAAACCCCTCA
GGATTGCCCTCTGGCCTGGGGAAAGAACACACCTGCAACCCTGATGAAGAACACGTGGTCG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGAACACCTCTGCTCTGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTCTGTGATGACAACACTGGGAGAAAAGGAGGA
CCAGGGTGTATGCAAGCAACTGGCTGTGGAAGTCCCTCTCCCTCAGAGACCGGA
AATGCTATGCCCTGGGTTGCCGCATCTGGCTGGATAATGTTGCTCAGGGAGGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTGGGGTTTCAGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGACTTAACTTGGTGCCTGATTCTCAGGCCTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGAACATACATCA
CCACCTTCCTATGTCTCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTAT
CAACTACTAAATACATTCTCACACACACACACACACACACACACACACACACACACATA
CACCAATTGTCCTGTTCTCTGAAGAACTCTGACAAAATACAGATTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGAATTGGTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTATTACAATAATAAGATAGCAC
TATGTGTTAAA

FIGURE 54

MALLFSLILAICTRPGLASPSGVRLVGGHLRCEGRVEVEQKGQWGTVCDDGWDIKDVAVL
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCRAVL
TQKRCNKHAYGRKPIWLSQLMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPDFDLRLVG
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIDL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACCGTCCGGACCGTGGCGGACCGTGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCCTGGG
CGTCTCGGCCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAAGGCCTACCTGCCGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGCCCGGAATGGTGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACACCAGTGG
TGTGGACAAGAGGGTATGGAGACAAACTACTTTGGCCCAGTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA
CTGTCTGCGTGGCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATCACCAGGGATGGATCTAGGTATGGAGTTATGGAC
ACCACACAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTAAGCCTCCCTGGCTGTTATCTCGAA
CTCTGGCTCTGGCTCTTCTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTGAGACTTTAATGGAGATTGTCTACAAGTGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA
AGCTTCTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAGGGCGCCGCACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCATGGCCCAACTTGTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKEAKVFYAAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAIVAAAAEILQCFGYVDIL
VNNAGISYRGTIMDTTVVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLA AVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKS KNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCCCACCGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAACACACCAAAACGCTCGCAGCCACAAAAGGGATGAAATTCTTCTGGACATCCTC
CTGCTTCTCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTATTCTAA
GAGGAGAAAATCAGTCACCGGCAGAACATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA
GACTGACTGCCATGAATTGCTAAACTAAAAGCAAGCTGGTCTCTGGGATATAAAATAAG
CATGGACTGGAGGAAACAGCTGCCAATGCAAGGGACTGGGTGCCAAGGTCATACCTTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTAATTGCACATTCTGGACTACAAA
GGCATTCTTCTGCAATGACGAAGAATAACCATGGCCATTGTCACTGTGGCTCGGCAG
CTGGACATGTCTCGTCCCCTTACTGGCTTACTGTTCAAGCAAGTTGCTGCTGTTGGA
TTTCATAAAACTTGACAGATGAACTGGCTGCCTACAAATACTGGAGTCAAAACAAACATG
TCTGTGTCCTAATTCTGAAACACTGGCTTCATCAAAATCCAAGTACAAGTTGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG
ATTTTATTCCATCTCTATAGCTTTTAACAACATTGAAAGGATCCTCCTGAGCGTT
CCTGGAGTTAAAAGAAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAAAGCACCTAGTTCTGAAAAGTGAATTACAGGTTAGGTTGATGTCATCTA
ATAGTGCAGAATTAAATGTTGAACCTCTGTTTTCTAATTATCCCCATTCTCAATA
TCATTGGAGGCTTGGCAGTCTCATTACTACCACCTGTTCTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTAGAGGTGACTTTAAGGAAAATGAAGAAAAGAA
CCAAAATGACTTATTAAAATAATTCCAAGATTATTGTGGCTCACCTGAAGGCTTGCAA
AATTGTACCATAACC GTTATTAAACATATATTATTATTGATTGCACTTAAATTGT
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTTCAGCTCTAAATAAAA
TGAAGGACTATCTAGGGTATTTCACAATGAATATCATGAACTCTCAATGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACTCACATTCCAATGCCAAACATTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGATTAAAG
GAGAATTGAGAGAAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA
AAA
AAA

FIGURE 58

MKFLLDILLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHIGRLTAYEFAKLKSK
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAEGDVSI
YTNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHV
SVPFLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTS
LGPTLEPEEVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCCACCGCGTCCGCGGACCGGTGGTCGACTAGTTCTAGATCGCAGCGGCCGCCGC
AGGGAGGAGCACCGACTCGCGCCGCACCCCTGAGAGAATGGTTGGTGCCATGTGGAAAGGTGATTG
TTTCGCTGGTCCTGTTGATGCCTGGCCCTGTGATGGGCTGTTGCTCCCTATACAGAAGT
GTTTCATGCCACCTAACGGAGACTCAGGACAGCATTATTCCTACCCCTAACATTGAAGC
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGTCGGCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTGGTTC
TTCCCAGCTCAGATAACGCCAGAACAGATGCCAGTAGTTCTCTGGCTACAGGGTGGGCC
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGGCCTATGTTGTCACAAGTAACATGA
CCTTGCCTGACAGAGACTTCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTACTGATGATAACCCACGGATATGCAGTCATGAGGACGATGT
AGCACGGGATTTATACAGTGCACTAATTCAAGTTCCAGATATTCCTGAATATAAAAATA
ATGACTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGGCCATTGCACACCTC
ATCCATTCCCTCAACCCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCCGAATCAATTATAGGGGGCTATGAGAACATTCTGTACCAAATTGGCT
TGTTGGATGAGAACGAAAAAAAGTACTTCCAGAACAGCAGTGCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTGAGGCCTTGAATACTGGATAAAACTACTAGATGGCAGCTAAC
AAAGTATCCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTGC
GCACGGAACCTGAGGATCAGCTTACTATGTGAATTTTGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGGAACATAGTTGAAAGTACTTGC
AGATAACAGTACAGTCAGTTAACGCCATGGTTAATGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAATGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCTGATGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTGGAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTACATCCGGCAAGCGGGTACCTCCATCAGGTAAATTATTC
GAGGTGGAGGCATATTTACCCATGACCAGCCTCTGAGAGCTTGTACATGATTAATCGA
TTCATTTATGAAAAGGATGGGATCCTTATGTTGATAAAACTACCTCCCCAAAGAGAACAT
CAGAGGTTTCATTGCTGAAAAGAAAATCGTAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTCATATCTGCAAGATTTTCATCAATAAAATTATCCTTGAAACAAGTGAGC
TTTGTGTTGGGGGAGATGTTACTACAAAATTAAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGAACAGATGTATAATGA
AATTTAGGGTCTTGAATAGGAAGTTTAATTCTTCTAAGAGTAAGTGAAGTGCAGTTG
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAACAGTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA
TAGTTTGGGAAAAGATTCTCAAATGTATAAAAGTCTTAGAACAAAAGAATTCTTGAAATA
AAAATATTATATAAAAGTAAAAAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPPKGDSGQPLFLTPYIEAGKIQKGRELSL
VGPFPGNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLRDRDPWTTLMSLYIDNPVGTGSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSILNPVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEIILDKLLDGDLTSDPSYFQNVTG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIIVAAALTERSLMGMDWKGSQEYKKAEKVVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTCCGGCTCCGAATGGCACATGTGGAATCCCAGTCCTGTTGGCTACAACAT
TTTCCCTTCTAACAAAGTTCTAACAGCTGTTCAACAGCTAGTGATCAGGGGTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTACCAGCTCCTT
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGGAGGGCCTGCCTAACAAAGCTTCAAAAACAGGAGCGACTTCACTGGCTGGGAT
AAGACGTGCCGGTAGGATAGGAAAGACTGGGTTAGTCCTAACATATCAAATTGACTGGCTGGG
TGAACCTCAACAGCCTTAAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTGTAAAATAAAATTAAAAAGCAAGTATTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAACAGAGGAGAAAGTATGTTAAAATA
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAACCACCAGGATGGGACCCCTGGGTC
AGGCCAGCCTTTGCTCCTCCGGAAATTATTGGTCTGACCACTCTGCCTGTGTTT
GCAGAACATGTGAGGGCCAACCAGGGAGGGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCGCTGGAGGTGG
ACAGCCGCTCTGGTCTGCTCAGTGGTCTGGGTGCTGGCCCCCCCAGCAGCCGGC
ATGCCCTAGTCAGCACCTTCACTCTGAGAACATCGTACTGGACCTCAACCACGGTACCGT
CCACCAAGGGACGGGGCCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTATAAGACAGGGCCAGAAGAGGGACAACAAGTCTCGTTACCCG
CCCCTCATCGTCAGCCCTGCAGCGAAGTGCTCACCCCTACCAACAATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGAGCCTCTACCAGGGGTCTGCA
AGCTGCTGCGGCTGGATGACCTTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGCACCATGTACGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCCCTGTCCA
GCCGGAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGCTCCCACTTGACAT
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCCGAGA
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTTCTACACCTCACGCATCGTCGG
CTCTGCAAGGATGACCCAAGTTCCACTCATACGTGTCCCTGCCCTCGGCTGCACCCGGC
CGGGGTGGAATACCGCCTCCTGCAGGCTGTTACCTGGCCAAGCCTGGGACTCACTGGCC
AGGCCTTCAATATCACCAGCCAGGACGATGTACTCTTGCCATCTTCTCAAAGGGCAGAAG
CACTACCGACCCGCCCCGATGACTCTGCCCCGTGTGCGCTCCCTATCCGGGCATCAACTT
GCAGATCAAGGAGCGCCTGCAGTCCTGCTACCAAGGGCGAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGAAGGACGTCCAGTGCACGAAGGGCCTGCCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTACAACGGCTACAGCGTGGTTTG
TGGGGACTAAGAGTGGCAAGCTGAAAAGGTAAGAGTCTATGAGTTAGCTATGAGGTTAGCT
ATTCACCTCCTCAGCAAAGAGTCCCTTTGGAGGTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTATTCTGGGAACAAAGGTGAAATGGGAGGTAAGAAGGGGTTAATTGTG
ACTTAGCTCTAGCTACTTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCCAAACTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSRSVVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLIIIDYSENRLLACGSL
YQGVCKLLRLDDLFIΛVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLP RDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFH SYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSL A QAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPRAINLQIKERLQSCYQGEGN
LELNWL LGKD VQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGCGGCTGAGTGC GGACTGGAGTGGGAACCCGGTCCCCCGCCTTAGAGAACACGCG**A**TGACCA
CGTGGAGCCTCCGGCGAGGCCGGCCCGCACGCTGGGACTCCTGCTGCTGGTCGTCTGGGCTCCTGGTGCCTC
GCAGGCTGGACTGGAGCACCTGGTCCCTCTGCGCTCCGCATCGACAGCTGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTCTGGATCTCGGGCTCCATCCACTATTCCTGTCGCCCAGGGAGTACT
GGAGGGACCGCCTGCTGAAGATGAAGGCTGTGGCTTGAAACACCCCTCACCACTATGTTCCGTGGAACCTGCATG
AGCCAGAAAGAGGCAAATTGACTTCTCTGGAACCTGGACCTGGAGGCCCTCGTCTGATGGCCGCAGAGATCG
GGCTGTGGTGTATCTCGCTCCAGGCCCTACATCTGCACTGAGATGGACCTCGGGGCTTGCCAGCTGGCTAC
TCCAAGACCCCTGGCATGAGGTGAGGACAACCTACAAGGGCTCACCGAAGCAGTGGACCTTATTGACCACC
TGATGTCAGGGTGGTGCCTCCAGTACAAGCGTGGGGGACCTATCATGCGTGCAGGTGAGAATGAATATG
GTTCTATAAAAGACCCGCATACATGCCCTACGTCAAGAAGGGACTGGAGGACCTGGCATTGGAACACTGC
TCCTGACTTCAGACAACAAAGGATGGCTGAGCAAGGGGATTGTCAGGGAGTCTGGCCACCATCAACTTGCACT
CAACACACGAGCTGCACTGACCACTTCTTCACAGTCCAGGGACTCAGGCCAAGATGGTATGGAGT
ACTGGACGGGGTGGTTGACTCGTGGGGAGGCCCTCACAAATATCTGGATTCTCTGAGGTTTGAAAACCGTGT
CTGCCATTGTGGACGCCGGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCCAACACTTGGCTTCATGAATG
GAGCCATGCACTTCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTCGACAGAACGCCGG
ATTACACGCCAAGTACATGAAGCTCGAGACTCTCGGCTCCATCTCAGGCATCCCTCCCTCCCCAACCTG
ACCTTCTCCCAAGATGCCGTATGAGCCCTAACGCCAGTCTGTACCTGTCCTGTGACGGGACGCCCTCAAGTACC
TGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGAAATGGACAGTCCT
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCAGTCATGATCGGGGCAGG
TGTGTTGAAACACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGATTGCTGTCCTTGATCCAGGGTT
ACACCGTGTGAGGATCTTGGTGGAGAATCGTGGGAGTCAGTCAACTATGGGAGAATATTGATGACCAGCGCAAAG
GCTTAATTGGAAATCTCTATCTGAATGATTCAACCCCTGAAAAACTTCAGAACTATAGCCTGGATATGAAGAAGA
GCTTCTTCAGAGGTTCGGCTGGACAAATGGNGTCCCTCCAGAAACACCCACATTACCTGCTTCTTCTGG
GTAGCTGTCCATCAGCTCACGCCCTGTGACACCTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTTGTATTCA
TCAATGCCAGAACCTTGGACGTTACTGGAACATTGGACCCAGAAGACGCTTACCTCCAGTCCCTGGTGTGA
GCAGCGGAATCAACCCAGGTATCGTTTGAGGAGACGATGGCGGGCCCTGCAATTACAGTCAGGAAACCCCC
ACCTGGGCAGGAACCAAGTACATTAAGT**G**CGGTGGCACCCCTCCTGCTGGTGCCAGTGGAGACTGCCCTC
CTCTTGACCTGAAGGCCCTGGTGGCTGTCGCCCCACCCCTCACTGCAAACAGCATCTCCTTAAGTAGCAACCTCAGGG
ACTGGGGCTACAGTCTGCCCTGTCAGCTCACAAACCTAAGCCTGCAAGGAAAGGTGGATGGCTCTGGGCC
TGGCTTGTGATGGCTTCTTACAGCCCTGCTCTGTGCCAGGGCTGTGGGCTGTCTCTAGGGTGGAGC
AGCTAATCAGATGCCCTAGCCTTGGCCCTCAGAAAAAGTGTGAAACGTCGCCCTTGCAACGGACGTACAGCCC
TGCAGCATCTGCTGGACTCAGCGTGTCTTGCTGGTCTGGAGGCCACATCCCTCATGGCCCCAT
TTTATCCCCGAATCCTGGGTGTGTCACCAGTGTAGAGGGTGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT
CTTCCTCACAACCTCTGAGCCTCTTGGATTCTGGAAGGAACTCGGCGTGAAGAACATGTGACTTCCCTT
TCCCTTCCCACTCGCTGCTTCCACAGGGTGACAGGCTGGAGAACAGAAATCCTCACCTGCGTCTTCC
CAAGTTAGCAGGTGTCTCTGGTGTCACTGAGGAGGACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGCA
CATCCAGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGCACATCCAGGG
AGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGCACATCCAGGG
GGAGGACAGAAGGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGCACATCCAGGGAGGAGG
ACAGAAGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCCAGGCCGAACAGCAGGGGAGAGCAGGCCCTCTTC
GAAGTGTGTCCAAGTCCGATTGAGCCTTGTGTTGGGCCCAGCCAACACCTGGCTTGGCTCACTGTCCTGA
GTTGCAGTAAAGCTATAACCTTGAATCACAA

FIGURE 64

MTTWSLRRR PART LGLLL VVLGFLV LRR LDWST LVPL RL RQL GLQAK GWN FMLED STFW
IFGGSIHYFRVPREYWRDRLLKMKACGLNTLTTYVPWNLHEPERGKFDFSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEAVDLYFDHLMMSRVVPLQ
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSNDNKGLSKGIVQGVLAT
INLQSTHELQLLTTFLFNVQGTQPQPKMVMEYWTGFDSWGGPHNILDSS EVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP
LPPPDPDLLPKMPYEPLTPVLYLSLWDALKLGEPIKSEKPINMENLPVNGGNQSFQGYI LY
TSITSSGILSGHVGHD RGQVFVNTVSIGFLDYKTTKIAVPLI QGYTVL RILV ENRG RVNYGEN
IDDQRKGLIGNLYLNDSP LKNFRIYS LDMKKSFFQR FGLDKWXSLP EPTPLPAFFLG SLSIS
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTL YLPGPW LSSG INQVIV FEETMAGPA
LQFTETPHLGRNQYIK

TOOTYFADQV*EDGEGEGEDG

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGCCCCAGGACC
CTGGTGAGGGTTCTACTTGGCCTTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGCTCGGCCCGAGGCCCGAGGACCTCCATCTCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCCCGTCTCAGACTAGAGGAGCGCTGTAAACGCC**ATGGCTCCC**
AAGAACGCTGTCTGCCTCGTCCCTGCTGCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGTCGTTCGTAGTGGATAGGGTCATGACCGTTCTCCTAGACGGGCC
CGTCCGCTATGTGTCTGGCAGCCTGCACTACTTCCGGTACCGCGGGTGTGCTTGGGCCAC
CGGCTTTGAAGATGCGATGGAGCGGCCAAGCCATACAGTTATGTGCCCTGGAACTA
CCACGAGCCACAGCCTGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCCTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCCATCTGGTTGCTTCGAAAACCTGAAATTCTAAGAACCTC
AGATCCAGACTTCCTGCCGAGTGGACTCCTGGTCAGGGTCTTGCCTGCCAAGATATATC
CATGGCTTATCACAATGGGGCAACATCATTAGCATTCAAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTGGCTGGCTCTCGTGCAGCTGCTAGG
AGAAAAGATCTTGCTCTCACACAGATGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGG
GAECTATACCACTGTAGATTTGGCCAGCTGACAACATGACCAAAATCTTACCCCTGCTT
CGGAAGTATGAACCCCATTGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA
CTGGGCCAGAATCACTCCACACGGTCTGTCAAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG
AATGGTGCCGATAAGAAGGGACGCTTCCTCGATTACTACCAGCTATGACTATGATGCCAC
TATATCTGAAGCAGGGACCCACACCTAACGTTTGCTCTCGAGATGTCATCAGCAAGT
TCCAGGAAGTTCTTGGGACCTTACCTCCCCGAGCCCCAAGATGATGCTGGACCTGTG
ACTCTGCACCTGGTTGGCATTACTGGCTTCTAGACTTGCTTGCCTCCGGGGCCCAT
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGTACC
GAACCTATATGACCCATACCAATTGGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTC
CATGACCGTGCCTATGTGATGGGATGGGTGTTCCAGGGTGTGGAGCGAAATATGAG
AGACAAACTATTTGACGGGAAACTGGGTCCAAACTGGATATCTGGTGGAGAACATGG
GGAGGCTCAGCTTGGGCTAACAGCAGTGACTCAAGGGCTGTTGAAGGCCACCAATTCTG
GGGCAAACAATCCTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTGTGAAGTG
GTGGTTCCCTCCAGTTGCCAAATGGCATATCCTCAAGCTCCTCTGGCCCCACATTCT
ACTCCAAAACATTCCAATTAGGCTCAGTGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGTTAACTTGGCCGGTACTGGACAAAGCAGGGCC
ACAACAGACCCCTACGTGCCAAGATTCTGCTGTTCTAGGGAGCCCTAACAAAATTA
CATTGCTGGAACTAGAACGATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGGACT**TGAAAGGTAGGCCGGCATGGCTCATGC**
CTGTAATCCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAGGACTTCAAGA
CCAGCCTGGCAACATGGTAAACCCGTCTCCACTAAAAATACAAAAATTAGCCGGCGTG
ATGGTGGGCACCTCTAACCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGACCACTGCACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVE
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLWQNHSTRVSATKGLENMLKLGASVNMYMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPGLPLPPSPKMML
GPVTIHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMHTIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRSLFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADETLSASEPMELSGH

Y007202 Y007203 Y007204 Y007205 Y007206

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTGAAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTGC
ACCCACAATATGGCATGTTGAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGATACTTGAAGGAATATT
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTTAGTGACATTCCAGATGTCAAAACGATTT
GCGTCCCTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAAGTTAGTGAAAATAAACTTAGGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTCAACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGGTGCCGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAAATTCTGCTAACGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAAACAGACTGCTTTAGCTTCGCGATCACTTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCCTGGTGTATTTGCTAAAAA
CCTTCGAGAGTTGTAACATTAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGGCGCACCTTAAGATTCTCCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTAACAAAGTTAGTCATTATAATGACGGCAC
TAAACTCTGGTACTGAAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAACAGGAACGGAT
TTAAAGTCCAATAACATTGCAATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT
GACTTGTAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTATTACCCATGTCA
AAAACTTGGAGTCACTTATTCCTAACACAAGCTCGAACCTTACCGAGTGGCAGTATT
AGTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAAACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC
CAAACAAATTGTTAAATGCATAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC
TCACCTCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGCCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGTTGTTG
TGGAAAGATCACCTTTGATAACCCCTGCCACTCGAACAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAAATGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AACTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG
ATACATCTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGTTAGGGTTAAGTCATTCAATTCAAATCATTGTTTTCTTTGGGG
AAAGGGAAGGAAAATTATAATCACTAATCTGGTTCTTTAAATTGTTGTAACGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTGCCGTCAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMNTNLQELHLCCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKLNRELVALIGNLNSENNKMGLESLRELRLHLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNCLDRPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCACCGCTCCGGCCTCTCTGGACTTGCATTCCATTCCCTTTCATTGACAACTGACTTTTTATTC
TTTTTCCATCTCTGGGCCAGCTGGGATCCTAGGCCGCCCTGGGAAGACATTGCTTTACACACATAAGGAT
CTGTGTTGGGTTCTCTCCCTGGACATTGGCATTGCTTAGTGGTTGTGGGGAGGGAGCACACGTGG
GCTCAGTGCTTGCACTTATCTGCCTAGGTACATCGAAGCTTTGACCTCCATACAGTGAATTATGCTGTC
ATCGCTGGTGGTACCTGGCTCTGGCTCTGCTGATAGTGTGCTCTGCTTACTTCAAATACACAAC
GCGCTAAAAGCTGCAAAGAACCTGAAGCTGTGGCTGAAAAAATCACAACCCAGACAAGGTGTGGTGGCCAAG
AACAGCCAGGCCAAACCATGCCACGAGCTTGCTCTGCAGTGTGAAGGATATAGAATGTGTGCC
AGTTTGATTCCCTGCCACCTTGCTGCGACATAATGAGGGCCTGAGTTAGGAAGGCTCCCTCAAA
GCAGAGCCCTGAAGACTCAATGATGTCATGAGGCCACCTGTTGTGATGTGCGAGCACAGAAGAAAGGCACAG
CTCCCCATCAGTTCATGGAAAATAACTCAGTGCTGCTGGGAACCAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGCAACCTTCCAGGAAGGAGTTGGGGAGAGAGAACCCACTGTGGGAATGCTGATAAACCAAGTCA
CACAGCTGCTCTATTCTCACACAAATCACCCCTGCGTGGCTGGAACGTGTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGGCCATAAAAGCTGTCGGCTTAAGGCTGCCAGGCCTGCCAAAATGGAGCTTGT
AGAAGGCTCATGCCATTGACCCCTTAATTCTCTGTTGGGGAGCTGACAATGGCGGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGTGCCAATATGGCAGAGACCCACAAGGCCATGATCCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAGACCAGAAAACAAAAGCATCAGAATTATCTTTCTATGTCCAGCTT
GATCCAGATGGAAGCTGTGAAAGTGAACATTAAAGCTTGAACGGAACTCCAGCAATGGGCTCTGCTAGGG
CAAGTCTGAGAAAAACGACTATGTTCTGTATTGAATCATCATCCAGTACATTGACGTTCAAATAGTTACT
GAECTCAGCAAGAATTCAAAGAACTGTCTTGTCTTCTACTACTTCTCTCCTAACATCTCTATTCAAACGT
GGCGGTTACCTGGATACCTTGAAGGATCCTCACAGCCCCAATTACCCAAAGCCGATCCTGAGCTGGTTAT
TGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTCAAAGAGATTTCCTAGAAATAGAC
AAACAGTGCACATTGATTTCTGCCATCTATGATGGCCCTCCACCAACTCTGGCTGATTGGACAAGTCTGT
GGCCGTTGACTCCCACCTTGAATCGTCACTCAAACACTCTGACTGTCGTGTTGTCTACAGATTATGCCAATTCT
TACCGGGGATTCTGCTTCTCACACCTCAATTATGCAAGAAAACATCAACACTACATCTTAACTTGCTTCT
GACAGGATGAGAGTTTATAAGCAAATCTACCTAGAGGCTTTAACTCTAAATGGAATAACTTGAACACTAAA
GACCCAACTTGCAAGACCAAAATTATCAAATGTTGGAATTCTGTCCTCTTAATGGATGTTGACATCAGA
AAGGTAGAAGATCAGTCATTACTACACCAATAATCACCTTTCTGCTCCTCAACTCTGAAGTGTACCC
CGTCAGAAACAACTCCAGATTATGTGAAGTGTGAATGGACATAATTCTACAGTGGAGATAATATACATAACA
GAAGATGATGTAATACAAAGTCAAAATGCACTGGCAAATATAACACCAGCATGGCTTTGAATCCAATTCA
TTGAAAAGACTATACTTGAATCACCATTATGTTGATTGAACCAAACCTTTTGTCAAGTTAGTCTGCAC
ACCTCAGATCCAAATTGGTGGTTCTGATACCTGTAGGCCCTCTCCACCTCTGACTTGCATCTCAACC
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAAACTTGTAAAGGTGATCCCTTATTGGACACTATGGGAGA
TTCCAGTTAATGCCCTTAAATTCTTGAGAAGTATGAGCTGTGATCTGCAGTGTAAAGTTGATATGTGAT
AGCAGTGACCAACCACTCGCTGCAATCAAGGTTGTCTCCAGAAGCAAACGAGACATTTCTCATATAATGG
AAAACAGATTCCATCATAGGACCAATTGCTCTGAAAAGGGATCGAAGTGCAGTGGCAATTCAAGGATTTCAGCAT
GAAACACATGCGGAAGAAACTCCAAACCCAGCCTTCAACAGTGTGCATCTGTTTCTCATGGTCTAGCTG
AATGTGGTACTGTAGGACAACTCACAGTGAGGCATTGTAAATCAACGGGAGACTACAAATACCAAGAAGCTG
CAGAACTATTAACTAACAGGCTAACCTAAGTGAGACATGTTCTCCAGGATGCCAAAGGAATGCTACCTCGT
GGCTACACATATTATGAATAATGAGGAAGGGCCTGAAAGTGACACACAGGCCTGCATGTAAAAAAA

FIGURE 70

MELVRRRLMPLTLLILSCLAEALTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIIFS YVQLDPDGSCES ENIKVFDGTSSNGPLLQVCSKNDYVPVFESSSTLT
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKDFLAIYDGPSTNSGLIGQVCGRVTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSIYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDV IQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFA SPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGC VSRSKRD ISSYWK TDSIIGPIRLKRDRSASGN SGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVT VATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCCGGAGCCTGCAGAGAGGACAGCCGCCCTGC
GGACTGCGGCCCGAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGC
TGCTGCCGCCGCCGTGCCCTGCCACAGCGCACCGCCTCGACCCCCACCTGGGAGTCC
CTGGACGCCGCCAGCTGCCGCCGTGGTTGACCAGGCAAGTCGGCATCTCATCCACTG
GGGAGTGTTCCTCGTCCCCAGCTCGGTAGCGAGTGGTTCTGGTGGTATTGGCAAAGGAAA
AGATAACCGAAGTATGTGGAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT
TTTGGACCACTATTTACAGAAAATTTTAATGCCAACCAAGTGGGCAGATATTTTCAGGC
CTCTGGTGCCAAATACATTGTCTTAACCTCCAAACATCATGAAGGCTTACCTTGTGGGGGT
CAGAATATTGTGGAACTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTGACTGTACTATTCCCTTTGA
ATGGTTTCATCCGCTCTCCTTGAGGATGAATCCAGTTCATCCATAAGCGGAATTCCAG
TTTCTAAGACATTGCCAGAGCTATGAGTTAGTGAACAACATATCAGCCTGAGGTTCTGTGG
TCGGATGGTACGGAGGAGCACCGGATCAAACTGGAACAGCACAGGCTCTGGCCTGGTT
ATATAATGAAAGCCCAGTTGGGGCACAGTAGTCACCAATGATCGTGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTGC
CATAAATGGAAAAGTGCATGACAATAGACAAACTGTCCTGGGCTATAGGAGGGAAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTCATGTG
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTCTGTAGTTTGAG
GAGCGACTGAGGCAAGTGGGCTCTGGCTAAAGTCAATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTTCCTAAATGGCCACATCAGGACAGCTGTTCTGGCCAT
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAAC
GATTTCTTGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCAGATGC
CGTGTAAATGGGCTGGCTAGCCCTAACTAATGTGATTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAAACTGGATAAGAAAATTATTGGCAGTTCAGCCCTTCCCTTTCCACTA
AATTTCCTTAAATTACCCATGTAACCATTAACTCTCCAGTGCACTTGCCATTAAAGTC
TCTTCACATTGATTGTTCCATGTGTGACTCAGAGGTGAGAATTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACGTGAAATTATGTTGAAGCCATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCATTGCTAGTCAAT
TTTTTTGTGCCAACATCATAGAGTGTATTACAAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTAGGTATAGACTGTTGCTCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAATACTGTAAAATAATGGTGCACCTGTATAGGGCACTTACCAAGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTATAAAACTGTATGCTTAGGCTACACTACATTATAAAAAAAA
GTTTTCTTCTTCATTATAAATTAACATAAGTGTACTGTAACTTACAAACGTTTAATT
TTTAAACCTTTGGCTTTGTAATAACACTTAGCTAAAACATAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFLPLLLLLLPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSPGSEFWWYWQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSGDGGAPDQYWNSTGFLAWLY
NESPVVRGTVVNTDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNNDTVTPDVWYTSPKKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWLALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGCCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGGCAGGTGTTCAGCCTGGTGTG
CTTCTCACTTCATCTGGACCACGAGGCTCTGGTCCAAGGCTCTTGCAGAAGAGCT
TTCCATCCAGGTGTATGCAGAATTATGGGATCACCCCTGTGAGCAAAAAGGCGAACAGC
AGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAACACTTGAGCTATGGCTGGGTTGGAGA
TGGATTCGTGGTCATCTCTAGGATTAGCCAAACCCAAAGTGTGGAAAAATGGGTTGGGTG
TCCTGATTTGAAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACATCTGAT
ACTTGGACTAACTCGTGCAATTCCAGAAATTATCACCACCAAAGATCCCATAATTCAACACTCA
AACTGCAACACAAACAAACAGAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCC
ACTCTACAATAACCTGCCCTACTACTACTCCCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAAATTGATTGTGTACAGAAGTTTTATGGAAACTAGCACCATGTCTACAGAAAC
TGAACCATTGTTGAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTGAGCTGGCTTGGATTG
TATGTCAAAAGGTATGTGAAGGCCTTCCCTTTACAAACAAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAGGAGGAGAAGGCCAATGATAGCAACCTAATGAGGAATCAAAGA
AAACTGATAAAACCCAGAAGAGTCCAAGAGCAAAACTACCGTGCATGCCTGGAA
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC
TTACCCCTGCCAGCTGGGAAATCAAAGGGCAAAGAACCAAAGAACAGTCCACCC
GGTCTCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC
CCTTCTCCTTATTGTAACCCGTCTGGATCCTATCCTCCTACCTCAAAGCTCCACGGCC
TTCTAGCCTGGCTATGCTCTAAATAATATCCCCTGAGGAGAAGGAGTTTGCAAAGTGCAA
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTGAGGCTAGG
TGGGTGAAAGCCAAGGAGTCAGTGAGACCAAGGCTTCTACTGATTCCGAGCTCAGAC
CCTTCTCAGCTCTGAAAGAGAAACACCGTATCCCACCTGACATGTCCTCTGAGCCGGTA
AGAGCAAAGAACATGGCAGAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAGCTAAAGAAATAGAACAAAGCTGAGGAGACAGTACACT
GTCAGCAGGGACTGTAACACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTTCTCT
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAATTCTATTGAGACTAATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGCAAGTGCTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTCA
GTTTGATATTCTAGCTTACTTCCAAACTAATTGTTATTGCTGAGACTAATCT
ATTCAATTCTCTAATATGGCAACCATTATAACCTAATTATTAAACATACCTAACAGAAG
TACATTGTTACCTCTATATACCAAAGCACATTAAAAGTGCCTAAACAAATGTACTA
GCCCTCCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTCAGAAATTTAA
AGCATTAGAAAACCTT

FIGURE 74

MARCFSLVLLTSIWTRLLVQ GSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNNPKCGKNGVGVLIWKPVSRQF
AAYCYNSSDTWTNSCIPEIITT KDPIFNTQTATQTTEFIVSDSTYVASPYSTIPAPTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKA AFKNEAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTGGCACCTCTAATTGCTCTCGTATTGGTGCACGACTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTCGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA
ACTGCCGCCGCTCTGCCACGGCTGCCACCCAACGCGAACAGCGTAACCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGAACATAAGGCAACATATTTCATGTTAGTAAAGTGGCCAACACAAT
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCATGATAAA
ACCATTGATGAGGAACATAGAACGGGACAAGAGGGTCACTTGGATTGGAGTTCTTGCCAA
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTGGAAAGGTGGATGTTGGACGCTACTGATGTTAGTACGGTAC
AAAGTGAGCACATCACCCCTACCAAGCAACTCCCTACCCGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTTCAACCCCCACACAGTGTCA
TGGGAAAACAAGAAGGATAAATAAGATCCTCACTTGGAGTGCTCCTCTCCTGTCAATT
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTGG
CTGNGACTGGNTGGGGCAGCATGCAGCTCTGATTAAAGAGGCATCTAGGAAATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGGCCAAGTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGGAAATGGTTCCCTCCAAGCTTGGTCAGTGTGTTACTGTTATC
AGCTATTGACACATCTCCATGGTTCTCCATGAAACTCTGTTGTTCATCATTCTTCTTAG
TTGACCTGCACAGCTGGTTAGACCTAGATTTAACCTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAATTTCCCCCAAGGACTCTGCTTCTTAAGCCTCTGGCTTATGGTC
TTCATTAAAAGTATAAGCCTAACTTGTGCTAGCCTAAGGAGAACCTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAACCCCCATTGGTGGGATTGAGAAGGGTGAA
TAGAGGCTTGAGACTTCCTTGTGGTAGGACTTGGAGGAGAACCTGGACTTTCAC
TAACCCCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAFLLVRKLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFPSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRACKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGGGCCCCGAGAGCTAGCCGTGAGGAGCTGCCTGGGACGTTGCCCTG
GGGCCAGCCTGGCCGGTCACCCTGGCATGAGGAGATGGCCTGTTGCTCCTGGTCCA
TTGCTCCTGCTGCCGGCTCCTACGGACTGCCCTCTACAACGGCTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCCTGTTCACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGGCGTGTGCGTGTCAAATGGTGAAGCT
GTCGGAGAACGGGCCAGAGAAGGACGTGCTGGTGGCCATGGGCTGAGGCACCGCTCCT
TTGGGACTACCAAGGCCGCGTCACCTCGGGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTCGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTCAATTGACGGCTGGAG
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGGAGCTGGGGGTGTGGTCTTCCTTACCAAGTCCCCA
ACGGGCGCTACCAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAAGCAGGCTGCCGTG
GTGGCCTCTTGAGCAGCTTCCGGGCTGGGAGGAGGGCCTGGACTGGTCAACGCCGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATGTTGCCCGGCAGCCCTGCCGG
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACGCCGCTGCACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCCCTGAGAAGCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC
AGCTCTTGCCGCTGGAAGTCCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCGTGGTTCACCCGATCCTAACTGTGGGCCCCAGAGCCTGGGT
CCGAAGCTTGCGCTCCCCGACCCGCAGAGCCGCTTGTACGGTGTACTGCTACCGCCAGC
ACTAGGACCTGGGCCCTCCCTGCCGATTCCACTGGCTGTGATTGAGTGGTT
CGTTTCCCTGTGGTTGGAGCCATTTAACTGTTTATACTTCTCAATTAAATTCT
TTAAACATTTTTACTATTTTGAAAGCAAACAGAACCCATGCCCTCCCTGCTCTG
GATGCCCACTCCAGGAATCATGCTTGCTCCCTGGCCATTGCGGTTTGCTGGCTCTG
GAGGGTTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGCAGAGTGGC
GGTGGCTGTCTAGAATGCCGCCGGAGTCCGGCATGGTGGGCACAGTTCTCCCTGCC
CAGCCTGGGGAAAGAAGAGGGCCTGGGGCCTCCGGAGCTGGCTTGGCCTCTCCTGCC
CACCTCTACTTCTGTGAAGCCGCTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTCAGGCAGGAAATCTGAGGGAAGGAAGAAACTCCCCTCCCGTT
TCCCTCTCGGTTCAAAGAATCTGTTGTCATTGTTCTCTGTTCCCTGTGTGG
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGCTATGACTGCCCTCGCCAA
AAA
AAA

FIGURE 78

MGLLLVPLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPLYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSGPR
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG**TG**GATGTGGCACCACAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGCGCCCCCTGAGGCACGCTCCCCATGATGACGCCACGGGAA
CTTCCAGTACGACCATGAGGCTTCCTGGGACGGAAGTGCCAAAGGAATTGACCAACTCA
CCCCAGAGGAAAGCCAGGCCGTCTGGGCGGATCGTGGACCGCATGGACCGCGCGGGGAC
GGCGACGGCTGGGTGTCGCTGGCGAGCTCGCGGTGGATCGCGCACACGCAGCAGCGGA
CATACGGACTCGGTGAGCGCGCCTGGACACGTACGACACGGACCGGACGGCGTGTGG
GTTGGGAGGAGCTGCGAACGCCACCTATGCCACTACGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCGAGG
CGACCAGGATGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCGAGG
AGTTCCCTCACATGCGGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGATCTGTACTCAGCCAGCCTGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTCCGGACTTCCGGATCTGAACAAGG
ATGGGCACCTGGATGGAGTGAGGTGGCCACTGGTGCTGCCCTGCCAGGACCGACCCC
CTGGTGGAAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAA
AGCGGAAATCCTGGTAATTGGAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACCGATGAGCTG**TG**AGCACCGCGCACCTGCCACAGCCTCAGAGGCCCG
CACAATGACCGGAGGAGGGGCCCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCGCAGGAG
GCAGATGCAGTCCAGGCATCCTCTGCCCTGGCTCTCAGGGACCCCTGGTCGGCTTC
TGTCCCTGTCACACCCCCAACCCAGGGAGGGCTGTCATAGTCCCAGAGGATAAGCAATAC
CTATTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTGGCCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCAAATCTGAGCCTCCACCATAGACTGAAACTCCCCT
GGCCCCAGCCCTCTGCTGGCCTGGCTGGACACCTCCCTCTGCCAGGAGGAATAA
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSPDAGPHQGRVHQAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDGRDGRVGWEELRNATYGHYAPGEFFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKGHLDGSEVGHVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTCCGACTCGGGCGAGCCGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCGGGCGCGGGTGCAGGGATCCCTGACGCCCTCTGTCCTGTTCTTGTCGCTCCAG
CCTGTCTGTCGTCGTTGGCGCCCCGCCCTCCCCGCGTGCAGGGGTTGCACACCGATCCTG
GGCTCGCTCGATTGCCGCCAGGCGCTCCCAGACCTAGAGGGCGCTGGCCTGGAGCAG
CGGGTCGCTGTGCCTCTCCCTCTGCCGCCGCCGGGATCCGAAGGGTGCAGGGCTCT
GAGGAGGTGACGCCGCCGGCCTCCGCACCCCTGGCCTGCCGCATTCTCCCTCTCCAG
GTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCCGCTCTGGCCTCGGTGTG
TGTCTGCTGCTGCCGGGCCGCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATG
TTTACACAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGCTGCC
CTCTTGAGGAATTCTCTGTGTATGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
GCTGCTGTCCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGGAGTCTATAGCCTACC
TGGTCGAGAAAACATTCCCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGAT
GGTCTGCTTCTTCACAGTAACAAAGGAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAACGG
CAATAAAGATTGTAACAGACATTGCATTCTGATTGATGGAAGCTTAATATTGGCAGC
GCCGATTAATTACAGAAGAATTGGTGGAAAGTGGCTCTAATGTTGGGAAATTGGAAACA
GAAGGACCACATGTGGCCTTGTCAAGCCAGTGAACATCCAAAATAGAATTACTTGAA
AAACTTACATCAGCCAAAGATGTTGTTGCCATAAAGGAAGTAGGTTCAGAGGGGTA
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGGTATTATTGATGGTGGCCTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTTCTTACACATGCCCAACTGGTTGGCACCCACAAAATACGTAAA
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAAGCAAGACCTGTTATAACT
CAGTGAACATTGCCCTTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCC
ATGCTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTGCACAGAT
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCAAGTTCACTGACTATAGCACCA
AAGAGAAATGTCTAGCTGTCATCAGAAACATCCGCTATATGAGTGGGAAACAGCTACTGGT
GATGCCATTCTCACTGTTAGAAATGTGTTGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCCTAGTAATTGTCACAGATGGCAGTCCTATGATGATGTCACAGGCCCTGCAGCTGCTG
CACATGATGCAGGAATCACTATCTTCTCTGTTGGTGTGGCTGGCACCTCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTCTTCACAAGAGAGTCAAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGTTAGAGATTCTTAGAATCCCAGCAAT
AATGGTAACATTGACAACAGAAAGAAAAAGTACAAGGGATCCAGTGTGAAATTGTATT
CTCATAATACTGAAATGCTTCTAGCATACTAGAATCAGATAAAAATTAAGTATGTCAAC
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCTCTGGTTACAATTACAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTCTAGAAACTCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTTCAACCATGCCTACTAAATGTACAGATATGCAA
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAA

FIGURE 82

MSAAWI PALGLGVCLLLLPGPAGSEGA APIA ITCFTRGLDIRKE KADVLCPGGC PLEEF SVY
GNIVYASVSSICGAAVHRGVISNSGGPV RVYSLPGRE NYSSVDANGI QSQMLSRWSASFTVT
KGKSSTQEA TGQAVSTAHPPTGKRLKKTPEKKTGNKDC KADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNKNFTSAKDVLFAI KEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKV VVVFIDGWPSDDIEEAGIVAREFGVN VFIVSVAKPIPEELG
MVQDVT FVDKAVCRNNNGFFSYHMPNWF GTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFR LM LEFVSNI AKTFE ISDIGAKIAAVQFTYDQRTEFSFTD YSTKENV LAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCCGCGCTCCGCACCCGCGGCCCGCCACCGCGCCGCTCCGCATCTGCACCCGCAGCCC
GGCGGCCTCCCGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGTCCAGTC
GGCGCGGGCTGCAGGGCGCAGAGCGGAG**ATG**CAGCGGCTTGGGCACCCCTGCTGTGCCTGC
TGCTGGCGGCGGGCTCCCCACGGCCCCCGCGCCGCTCCGACGGCACCTCGGCTCCAGTC
AAGCCCGGCCCGCTCTCAGCTACCGCAGGAGGAGCCACCCCTCAATGAGATGTTCCCGGA
GGTTGAGGAAGTGTGGAGGACACGCAGCACAAATTGCGCAGCGCGTGGAAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCCAGCTAT
ACAATGAGACCAACACAGACAGAAGGGTGGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGCCAGCAGC
ATGTAUTGCCAGTTGCCAGCTTCACTACACCTGCCAGCCATGCCGGGGCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTCTGGGTCACTGCACCAAAA
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG
TGCTGTGCCTTCCAGAGAGGGCCTGCTGTTCCGTGTGCACACCCCTGCCGTGGAGGGCGA
GCTTGCATGACCCGCCAGCCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG
GAGCCTTGGACCGATGCCCTGTGCCAGTGGCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTCGTGGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCACTGGAGGGTGCAGCAGGAGCTGG
AGGACCTGGAGAGGAGCCCTGACTGAAGAGATGGCCTGGGGAGCCCTGCCGGCTGCCGCT
GCACTGCTGGAGGGAGAGATT**TAG**ATCTGGACCAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTCCCCAGGTGTGCTTAGCGTGGCTGACCAAGGCTTCTTCCCTACA
TCTTCTTCCCAGTAAGTTCCCCCTGTGCTTGACAGCATGAGGTGTGTCATTGTTCA
TCCCCCAGGCTGTTCTCAGGCTTCAGTCTGGCTTGGGAGAGTCAGGCAGGGTTAAC
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACCACTGGCAG
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGGAGGAGATGAAACAATGTGG
AGTCTCCCTTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAAACATCAA
CCTGGCAAAATGCAACAAATGAATTTCACGCAGTCTTCCATGGCATAGGTAAGCTG
TGCCTTCAGCTGTTGAGATGAAATGTTCTGTCACCCCTGCATTACATGTGTTATTCA
AGCAGTGTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT
CCTCTCTCAGCACAGCCTGGGGAGGGGTCAATTGTTCTCCTCGTCATCAGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTTGCCTAACAGTCACACAGCTAGTGAAGACAGAGCAGTT
CTGGTTGTGACTCTAACGCTCAGTGCTCTCCACTACCCACACCAGCCTGGTGCACCAA
AAGTGTCCCCAAAAGGAAGGAGAATGGATTGTTGAGGCATGCACATCTGAAATTAG
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCCGTCTTAATGAAGACAATGATATTGACACTGTCCCTTTGGCAGT
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAACA
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTGCAAATCACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACCTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTTACCATCCAGAGTTAAAGTTAAAGTGTGCACATGATTGTA
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTTGCATTTAGAAATCAAGC
ATAAAATCACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAKASSEVNLANLPPSYHNETNTDTKGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRSHECIIDEDCGPSMYCQFASFQYTCQPCRQMLCTRSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGGLCCAFQRGLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAALLGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGGCTGGGAGGAAGAGGTAAGAAAGGTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCTG
AAGATAACAATAATTTCAGCCATCCACTCTCCTCCCTCCAAACACACATGTGCATGTACACACACACATACA
CACACATACACCTCCTCTTCACTGAAGACTCACAGTCACTCTGTGAGGAGGTGAGTCATAGAAAAGGACAC
TAAAGCCTTAAGGACAGGCCATTACCTCTGAGCTCCTTGCTTGTGACTCAAACATGGGAGGG
CCAGGCACGGTACACACTGTAATCCCAGCATTTGGGAGACGGAGGTGAGCAGATCACTTGAGGTGAGGAG
TTCGAGACCAGCCTGGCAACATGGAGAAACCCCCATCTACTAAAAAATACAAAATTAGCCAGGAGTGGTGGC
AGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGAATCGCTGAATCCAGGGGGGAGGATGCAGT
CAGCTGAGTGCACCGCTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACAAACAGGGAGGA
GGGGTAGATACTGCTTCTGCAACCTCTTAACCTGCATCCTCTTCCAGGCTGCCCTGATGGGGCTG
GCAATGACTGAGCAGGCCAGCCCCAGGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGA
GCCCCCGGTGTTCCCTGGGCCCTGGCAGGGTTGCTGACCCCTACCCCTGCAAACACACA
GTGAGAATGACTGCCCTGGGAGGGTGGTCCCTGGGCCCTGGCAGGGTTGCTGACCCCTACCCCTGCAAACACACA
AAGAGCAGGACTCCAGACTCTCCTTGTGAATGGTCCCTGCCCTGCAGCTCCACCATGAGGCTTCTGGGCCCC
ACTCTGCTAGCTGGTGGCTGGTGCAC TGCCACTGTGCCGTGGTACCCCTGGCATGTTCCCTGCC
GTGTCCTGCCAGATCCGGCCCTGGTATACGCCCGCTCGTCTACCCGGAGGCTACCAACTGTGGACTGCAATGA
CCTATTCTGACGGCAGTCCCCCGGCACTCCCCGCAGGCACACAGACCCCTGCTCTGCAAGAGCAACAGCATTGT
CCGTGTGGACCAGAGT GAGCTGGCTACCTGGCAATCTCACAGAGCTGGACCTGTC
CCAGGGCAACAGCTTCTGGGCCAGCCTGCTGAGCCTAGAGGAGAACCGAGCTGACCCGG
GGAGGACACAGCTTGCAAGGCTGGCAGCCTACAGGAACCTATCTAACCAACCAGCTTACCGCAGTC
CCCCAGGGCTTTCTGGCTCAGCAACTGCTGCCGCTGCAACTCCAACCTCTGAGGGCATTGACAG
CCGCTGGTTGAAATGCTGCCAACCTGGAGATACTCATGATTGGCGGAACAAGGTAGATGCCATCTGGACAT
GAACCTCCGGCCCTGGCCAACCTGCGTAGCCTGGTCTAGCAGGCATGAACCTGCGGGAGATCTCCGACTATGC
CCTGGAGGGCTGCAAAGCCTGGAGAGGCTCTTCTATGACAACCAGCTGGCCCGGGTGCCAGGCGGGCACT
GGAACAGGTGCCGGCTCAAGTCTAGACCTAACAGAACCCGCTCAGCGGGTAGGGCCGGGGACTTTGC
CAACATGCTGCACCTTAAGGAGCTGGGACTGAACAAACATGGAGGAGCTGGTCTCCATCGACAAGTTGCC
GAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTCTCCTCATCCACCCCGCGCCTTCCA
CCACCTCCCCAGATGGAGACCCCTATGCTCAACAAACAGCTCTCAGTGGCTTGACCCAGCAGACGGTGGAGTC
CCTGCCAACCTGCAAGGAGGTAGGTCTCACGGCAACCCCATCGCTGTGACTGTGCTATCCGCTGGCCAATGC
CACGGGCAACCGTGTCCGTTCATGAGCCGAATCCACCCCTGTGTGGAGGCTCCAGCAGCTCCAGCGCCTCCC
GGTCCGTGAGGTGCCCTCCGGAGATGACGGACACTGTTGCCCTCATCTCCCCACGAAGCTCCCCCAAG
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTCTGATTGCCGGCACTGGCGAACCGAGATCTACTG
GGTCACTCCAGCTGGCTTCTGACTGACACCTGCCATGCAAGGAGGTACCGGGTAGCCGGAGGACT
GGAGCTGGAGGGTGCAGCAGAGAGGAGGGCTATACACCTGTGTGGCCAGAACCTGGGGGCTGACAC
TAAGACGGTTAGGTGGTTGTGGCGTGCTCTCCCTCAGCCAGGCAGGGAGCAAGGAACAGGGCTGGAGCTCC
GGTGCAGGAGACCCACCCCTATCACATCTGCTATCTGGGTCAACCCACCCACAGTGTCCACCAACCTCAC
CTGGTCCAGTGCCTCCTCCCTCCGGGCCAGGGGCCACAGCTCTGGCCGCCTGGGAACCCACAGCTA
CAACATACCCGCTCTTCAGGCCACGGAGTACTGGGCTGCCGTGCAAGTGGCCTTGTGATGCCACACCA
GTTGGCTTGTGATGGGCCAGGACAAAGAGGCCACTTCTGCCACAGAGCCTTAGGGGATGTCCTGGCTCAT
TGCCATCTGGCTCGCTGCCCTCTGGCAGCTGGCTAGCGGCCACCTTGGCACAGGCCAACCCAGGA
GGTGTGGTGGAGGGCCCTCTCCCTCCAGCCTGGCTTCTGGGCTGGAGTGCCCTTCTGTCCGGTTGT
GTCTGCTCCCTCGCTGCCCTGGAAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGGAGACACTGTTGCC
ACCATTGTCTCAAATTCTGAAGCTCACCTGCTTCTGAGCAGTAGAGAAATCACTAGGACTACTTTTACCAA
AGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGGACCCACGTGCTGAGGCCAGCTGGC
CAAGACAGATGGGCTTTGTGGCCCTGGGGTGTCTCGAGCCTTGAAGGGCTTACCTCCTAGGGTCA
CCTCTGCTGCCATTCTGAGGAACATCTCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCTGCC
CTCTCTGCCAGAGGCTCTGGCTGGCTGTCCCCTACCTGTGTCCCAGGCTGCACCCCTTCTTC
TCTTCTCTGTACAGTCTCAGTTGCTCTGTGCTCTGGCAAGGGCTGAAGGGAGGCOACTCCATCTCAC
CTCGGGGGCTGCCCTCAATGTGGAGTGACCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAA
CGCCTCATCTCAGCAGCCTGGCTGGCATTCCGAAGCTGACTTTCTATAGGCAATTGTACCTTGTGAGGAA
ATGTGTACACCCCCAACCGATTCACTCTTCTCTGTAAAAAATAAAAATAAAATAACAATAAA
AAAA

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLQQSNSIVRVDQSELGYLANLTLDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQEYLHNQLYRIAPRAFSGLSNLLRLHNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMDNFRPLANLRSVLAGMNLREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGKFLDLNKNPLQRVPGDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHLPQMETLMLNNNALSAHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPLSQ
VASGESMVLHCRALAEPEIYWVTPAGLRLTPAHAGRYYRVYPEGTLELRRVTAAEAGLYT
CVAQNLVGDATKTVSVVGRALLQPGRDEGQGLELRVQETHPYHILLSWTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLAHLGTGQPRKGVGRRPLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLPSSGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

FIGURE 88

MRQTIIKVIKFILIIICYTVYYVHNIFDVDCVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQLNLNNNEWTLDKLQRQLTKNAQDKLELHLFMLSGIPDVTVDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLLRENLRALHIKFDTIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHLGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGCGCTCTCCCGT
CCCGCGGTGGTGCTGCTGCCGTGCTGGCCTGAACGCAGGAGCTGTCAATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGGCGTTCTAGCACTGGATTGGAAACTTGGAGGAAATTGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT
GTGGATAATCCCGTGGCACTGGGTTCAAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTCAGACATGATGGTTCTCCTGAAGACCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTCCATTCTACATTTCTCAGAGTCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCGAGGGACCATCAAGTGCAACTTGCAGGGGT
TGCCTTGGGTGATTCCCTGGATCTCCCTGTTGATTGGTGCCTCCTGGGACCTTACCTGT
ACAGCATGTCTCTCGAACAGACAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAGCACTCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTGTCTTGTAGCGC
CACGTGAGACACCTACAAACGAGATGCCTTAAGCCAGCTCATGAATGCCCATCAGAAAGAA
GCTCAAAATTATTCCCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGTAAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATAACCAGGGTCAGGAGGCCTG
GGTGCAGAAACTGAAGTGGCCAGAACTGCCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCCCTGT
ACAGTGACCCCTAAATCTTGGAAACATCTGCTTTGTCAAGTCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCAATGGTCTTGTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTACTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGGCTGTGATCAAGAACGGTCTGACCAGCTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTATTCTGCTTCTTAAAAACCTAAGATTTTAAAAAATTGAT
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELGKAEMIIEQNTDGVNFYNLTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTGGCCGTGGCA
GGGGAGCCTGCGCTGTGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGCGCACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTGGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCAACCTATGACATTG
CCTTGGTGAAGCTGTCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTGCCATCATAAACAA
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG
GTTTGTGCTGGCAACGCCAAGGGGGAGGATGCCTGCTGGTACTCAGGTGGACCC
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCGGTGTACACCAATATCAGCCACCACTTGAGTGGATCCAGAAG
CTGATGGCCCAAGAGTGGCATGTCCCAGCCAGACCCCTCCGGCCACTACTCTTTCCCT
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTTCTTCTGTCTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW
DSHVCVSVLLSHRWALTAACFETYSDLSDPSGMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEJVQVAINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCACCGCGTCCGGACGCGTGGGAAGGGCAGAAATGGGACTCCAAGCCTGCCTCTAGGGCT
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCCAGGCCGACCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGTCCCTGGCGTGCGGACCCCTGAGGAAGAGCTGAGTCTCACCTT
GCCCTGAGACAGCAGAATGTGAAAAGACTCTCGGAGCTGGTGCAGGCTGTGTCGGATCCCAG
CTCTCCTCAATAACGAAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC
CACTGACCCCTCCACACGGTGCAAAATGGCTTTGGCAGCCGAGCCCAGAAGTGCCATTCT
GTGATCACACAGGACTTCTGACTTGTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTCATCACTATGTGGAGGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC
ATCCCTACCAGCTTCCACAGGCCCTGGCCCCCATGTGGACTTTGTGGGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGTAACCCCTCTGTGATCCGAAGCGATAACAACCTTGACCTCACAGACGTGG
GCTCTGGCACCAAGCAATAACAGCCAAGCCTGTGCCAGTTCTGGAGCAGTATTCCATGAC
TCAGACACTGGCTCAGTCATGCGCTCTCGGTGGCAACTTGCACATCAGGCATCAGTAGC
CCGTGTGGTTGGACAACAGGGCCGGGCCGGGATTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGTGGGCCAACATCTCACCTGGGCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTTCCCTGAGTGGCTCATGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCTACATCCAGCGGGTCA
ACACTGAGCTCATGAAGGCTGCCGCTCGGGGCTCACCTGCTCTCGCCTCAGGTGACAGT
GGGGCCGGGTGTTGGCTGTCTCTGGAAAGACACCAGTTCCGCCCTACCTTCCCTGCCCTCCAG
CCCCTATGTCACCACAGTGGGAGGCACATCCTCAGGAACCTTCTCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTCAGCAATGTGTTCCCACGGCCTTCATACCAGGAG
GAAGCTGTAACGAAGTCCCTGAGCTCTAGCCCCCACCTGCCACCATCCAGTTACTTCAATGC
CAGTGGCCGTGCCCTACCCAGATGTGGCTGCACTTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGCCCATTCATGGTGTCCGGAACCTCGGCCCTACTCCAGTGTGTTGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTAGTGGCCGCCCCCTCTGGCTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGCAGGTCTTTGATGTAACCGTGGCTGCCATGAGTCCTGTC
TGGATGAAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGATCCTGTAACAGGC
TGGGAAACACCAACTCCCAGTTGCTTGAAGACTCTACTCAACCCCTGACCCTTCCATAC
AGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAGTTCACTGCCCCATTCTGCCCTGTTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCTGAAA
TGCTGTGAGCTGACTTGACTCCCAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCCTAGATTCCCTCAATAAGATGCTGTAACTAGCATTGATGCCCTCTCCCTCCGC
ATCTCATCTTCTTTCACTCAGGCTTTCAAAGGGTGTATAACAGACTCTGTGCACTA
TTTCACTTGATATTCACTCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT
TTCCTACCCCTGACATCCAGAAACAAATGCCCTCCAGTGCATACTTCTCAATCTTGCTTATG
GCCTTCCATCATAGTTGCCACTCCCTCCTACTTAGCTCCAGGTCTTAACCTCTCTG
ACTACTCTTGTCTCCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTG
TCCATTGAGATTTGTCTTCTCAGTTACTCATTGCTCCCTGGAACAAATCACTGACA
TCTACAAACCATACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATAACCTCAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGLHRFPPSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSDVGSGTSNNSQACAFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLFASGDGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESDLDEEVEGQGFCSGPWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GGCGCGCTCTCTCCGGCGCCCACACCTGTCTGAGCGCGCAGCGAGCCGGCCGGC
GGGCTGCTGGCGCGAACAGTGTGCTGGCATGGCAGGGATTCCAGGGCTCCTTTCTTC
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTTG
GCCTGCATACCGCCTCCCTGTCGTCTGCCAGTCTACCCCTCAATTAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCCAGTGTATAAGGGAAC
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTATGCCAATGG
CAGCCGACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAGGACTTCCTGCTCAACTACCCCTTCTAACATCAGTGAAGTT
ATCCACGGGCTGCACCGCACCCCTGGTGGCAGAGAACGATGCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAACGCTTCAGCCATGCCAGATGAA
AAGTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCAGATGAA
ATTCAGTGGATCCGGGTGAAACGCACCCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCTGGAACCTCAAAAGCCCCACAAGAGAAA
TTTATGAAGATTGGGGTGAGCCCTCCTGCTAACGAGCTGCCAGGGGCAGAACATTCACTCTC
TGGTTATGACAATGACCGACCAGGAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCTCTACCAGCAATGCGATGCCAGCCAGGGCCAGCGGGCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAACGTTGGAGCGAAAAATTATTGGCTTTTCAGG
GCACCAAGTGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAATCACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG
TGACACAGTGGTCCCTCTGGCAGCAATTAGGGTCTTGTGTTCTTATTTAGGAGAGGCC
AAATTGTTTTGTCAATTGGCGACACGTGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTGAAACTG
GTTTGTGTATCATATCATATCATTAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAACTGATTGGGCAATGAGGAATATTGACAATTAGTTAATCTTCACGTTTG
CAAACTTGATTTCATCTGAACCTGTTCAAAGATTATTAATATTAAATATTGGCATA
CAAGAGATATGAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSETLYANGSRTETQVGIYILSSSGDGAQHRD
SGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHV
LTAACIH
DGKTYVK
TQKLRVGFLKP
KFKDGGRGANDSTS
SAMPEQM
KFQWIRVKRTHVPKG
WI
KG
NANDIGMDYD
YA
LLELKPKH
RK
KFM
KIG
GV
SPPA
KQLPG
GR
IH
FSGYD
NDR
PGNLV
YRFCDV
KDE
TYD
LLYQQCD
AQPGASGSGVYV
RMW
KRQQQ
KWER
KI
IGIFSGH
QW
VDMNG
SPQDFN
AVR
ITPL
KYA
QICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCACCAGCCATGGTGGTTT
CTGGAGCGCCCCCAGCCCTGGGTGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGCGGCCAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTTGCTCACCAAGCCGCTGGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACTGTTCTTGCTGCTGCTGGG
GGCCTGGCAGCTGGGAACCCCTGGCTCTCGTCCCAGAAGGTGGGTGTTGCCTGGTGGAGC
CCCACCCCTGTGATTCCCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCAGGTCCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTCCCTTGC
CCCACCCCTCAGACCCTGCAGAACAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCAGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCAGCGAACAGGCC
GGGTCTACATCAGCCTCTGCGCACCGCTCTGGTGGAGAACATCGTCAAGGGGTGCA
GCTCCGCGGCGCCTCAGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCG
CCGCGCGCTCCTAGGGCCCAGCGGGACGCCGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGCGCCCTCGGCGTTCCCGCCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCGGACGGCTGCTGGGAAAGGAAACCCCTCCCCGACCCGCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCGCCAACGGCCTCATGTCCCCGCCAAC
GACTTCCGGCCCCGCCCGGGCCCCAGCGCTTTGTGTATATAATGTTAATGATTTTAT
AGGTATTTGTAACCCTGCCACATATCTTATTTATCCTCCAATTCAATAAAATTATTATT
CTCCAAAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLF SVLLGA WQLGNPGSRSQKVGVVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPI CLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPI IDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGI ISWGEGCAERNRPGVYISLSAHR SWEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGCCACCATGCACGGCTCCTGCAGTTCTGATGCTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGCCAGGTATCCCCGACGCCCTCACAGATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCTCGCAAGGCCTACGCACGGCAGTGCGTGTGGGCCAC
AACAAAGGAGCGCGGGCGCCGCGAGAATCTGTCGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGGCGTGGACTACAAACCTCAGGCCGCCACCT
GCAGCCCAGGCCAGATGTGCCACTACACGCAAGGTGGTATGGCCAAGACAGAGAGGATC
GGCTGTGGTCCCACCTCTGTGAGAAGCTCCAGGGTGGTGGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC
CGTGCCTCCAAATGTCCTCTGGCTACCACTGCAAGAACTCCCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTGCCTTACCTGGTAAC TGAGGCCCATCCTCCGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTCTCCCTAGCAACGGGATTCCGGCTTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCATGGCAACAGAGGCTCCACCTGCGTAAC
AACTGAGGTCCCTCCATTGGCAGCTCACAGCCTGCCCTCTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTCCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCTGACAGGGCAAG
GGAACCTCCTACCCATGCCAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCCTCAGTG
AGGTCTTGCCTCAGTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCAATACTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCGTCCTGCCAGGTGCAGAGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGCCCTGGTCATGTGTGGGCCCTCCTGGGA
CTACTGCTCCTGCCTCCTGGTGTGGCTGGAATCTTCTGAATGGGATACCACTCAAAGGG
TGAAGAGGTCA GCTGTCCTCTGTCA TCTTCCCCACCCCTGTCCCCAGCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCCGAAGGGAAAGGCTACGGGCATGTGCCCTCATCACACCCTCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACC
GGGCCACACCTCTCCTGCCCTCCCTCCTGAGTCCTGGGGTGGAGGATTGAGGGAGCT
CACTGCCTACCTGGCCTGGGCTGTCTGCCACACGATGTGCGCTCTCCCTGAGTGCCTG
TGTAGCTGGGATGGGATT CCTAGGGCAGATGAAGGACAAGGCCCACTGGAGTGGGTTC
TTTGAGTGGGGAGGCAGGGACGGAGGAAAGTAACCTGACTCTCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLLPLLLLVATTGPVGALTDEEKRLMVELHNLRYRAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVCWGHINKERGRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEADAQDLPYLVTTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCTEVPSILAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPGHVWGPLLGLLLPPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACGTGAAGTCAGGCTTTCATTTGGGAAGCCCCCTCAACAGAATTGGTCATTCTCCAAGTTATGGTGACGT
ACTTCCTGTTCTCCCTCGCTTGCCTTCAACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTCAT
CAAGGCAAGTCCATGCCAACCTCAAAGCCTCGAGAAGTGAACAACTGAATTGGAGACCATTCC
AAATCTGGGACCAAGTCTGCCAAATATTACACTCTCTCGCTGGAAAACAGGATTGGTGAACAAACTCCCTGA
ACATCTGAAAGAGTTTCAGTCCCTGAAACTTGGACCTTAGCAGCAACAATATTCAAGAGCTCCAAACTGCATT
TCCAGCCCTACAGCTCAAATATCTGTATCTCACAGCAACCGAGTCACATCAATGGAACCTGGTATTTGACAA
TTTGGCCAACACACTCCTGTGTTAACAGTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTAACT
GCCCAACTGCAACATCTCGAATTGAACCGAAACAGATTAAAAATGTAGATGGACTGACATTCAAGGCCCTGG
TGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAA
CATGGAAATTTGAGCTGGACCATAACAAACCTAACAGAGATTACCAAAAGGCTGGCTTACGGCTTGCTGATGCT
GCAGGAACCTCATCTCAGCCAAATGCCATCACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAAGCTCAG
TGAGCTGGACCTAACCTTCATCAAGGTTAGATGATTCAAGCTCCTGGCCTAAGCTTACTAAATAC
ACTGCACATTGGAAACAACAGAGTCAGCTACATTGCTGATTGCTTCCGGGGCTTCCAGTTAAAGACTTT
GGATCTGAAGAACATGAAATTTCCTGGACTATTGAAGACATGAATGGTCTTCTGGGCTTGACAAACTGAG
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTCACTGGTTGGATGCATTGGAGCA
TCTAGACCTGAGTGACAACCGCAATCATGCTTTACAAGGCAATGCATTCAAAATGAAGAAACTGCAACAAATT
GCATTAAATACATCAAGCTTGTGCGATTGCGCTAAATGGCTCCACAGTGGTGGGGAAACAACTT
TCAGAGCTTGTGAAATGCCAGTTGTGCCCATCCTCAGCTGCTAAAAGGAAGAAGCATTGGCTGTTAGCCCAGA
TGGCTTGTGTTGATGATTTCACCCAAACCCCGAGTCAGGGCTGCCAGAAACAGTCGGCAATAAAAGGTT
CAATTGAGTTTCATCTGCTCAGCTGCGAGCAGTCAGTGGCTTGGGAAAGACATGA
ACTACTGCATGCTGAAATGGAAAATTATGCCACACCTCCCCCAGGGTGGCAGGTGATGGAGTATAC
CATCCCTCGGCTGCGAGGTGAAATTGCGAGTGGAGGGAAATATCAGTGTGTCATCTCAACTTGGTTC
ATCCTACTCTGTCAAAGCAAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCATGGATCTCACC
CCGAGCTGGGCCATGGCACGCTGGAGTGCTGCTGGGACCCAGCCCCCAGATAGCCTGGCAGAAGGA
TGGGGCACAGACTTCCAGCTGCACGGGAGAGACGCATGCTGATGGTGGAGGATGACGTGTTCTTATCGT
GGATGTGAAGATAGAGGACATTGGGGTACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTCAGCAAATGC
AACTCTGACTGTCCTAGAAACACCATATTGGCGGCCACTGTTGGACCGAAGTGAACCAAGGGAGAAACAGC
CGTCTACAGTGCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACCTGGACCAAGATGATAGCCATTGGTGG
AACCGAGAGGCACTTTTGAGCAGGCAATCAGCTCTGATTATTGGACTCAGATGTCAGTGTGCTGGAA
ATACACATGTGAGATGTCACACCCCTGGCACTGAGAGAGGAAACGTCAGCTCAGAACAGTGCAGGAAGTATT
CTGCGACTCCCCCTCAGATGACAGCCCATCGTTAGACGATGACGGATGGGCCACTGTTGGTGTGCTGATCATGC
CGTGGTTGCTGTTGCTGGCACGTCACTCGTGGGTGCTCATCATACACACAAAGGGAGGAATGAAGA
TTGCAGCATTACCAACACAGATGAGGACCAACTTGGCAGAGTATTCTCTAGTTATTGTCATCTCAGGGAAACGTT
AGCTGACAGGGAGGATGGTACGTCTTCAGAAAGTGGAAAGGCCACCCAGTTGTCAGATCTCAGGGTGTGG
ATTGGTGGACTCAGTGAAGCTGATGTGGAAAGCTGC
CACAGATCTGTTCTTGTCCGTTGGATCCACAGGCCCTATGTTAGGGAAATGTGTATGGCTCAGA
TCCTTTGAAACATATCATACAGGTTGCAGTCTGACCCAGAACAGTTTAATGGACCAACTATGAGCCAGTT
CATAAAGAAAAGGAGTGCCTACCCATGTTCTCATCTTCAGAAGAACCTGCGAACGGAGCTCAGTAATATAC
GTGGCCTTCACATGTGAGGAAGCTACTAACACTAGTTACTCTACAATGAAGGACCTGGAAATGAAAATCTGTG
TCTAAACAAGTCTCTTGTGAAATTAGTGCACATCCAGAGGCCAGCGTGGTTGCCTCGAGTAATTCTTCATGGG
TACCTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTGGACAGCCATCAGATTGTCAGCC
AAGAGCCTTTATTGAAAGCTCATTCTCCCCAGACTGGACTCTGGTCTGGAGGAAGATGGAAAGAAAGGAC
AGATTTCAGGAAGAAAATCACATTGACCTTAAACAGACTTAAAGAAAACAGTCCAAATTTCAGTC
TTATGACTGGACACATAGACTGAATGAGACCAAGGAAAAGCTTAACATACACTACCTCAAGTGAACCTTATT
AAAGAGAGAGAATCTTATGTTTAAATGGAGTTATGAAATTAAAGGATAAAATGCTTATTGATACAGAT
GAACCAAAATTACAAAAGTTATGAAATTAAATGATGCTCATATAAGAACATACCTTTAAACTA
TTTTTAACCTTGTTTATGCAAAAAGTACTTACGTAATTAAATGATGATTATTGATTGTTATGTT
TTATAATGCCAGATTCTTTATGGAAAATGAGTTACTAAAGCATTAAATAACCTGCCTGTACCATTT
TTAAATAGAAGTTACTTCATTATATTGACATATTAAATAAAATGTGCAATTGAA

FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRIASIPPKMFKLPQLQHLELRNKKIKNVGGLTFQGLGALKSLKM
QRNGVTKLMGAFWGLSNMEIILQLDHNNLTEITKGWLGYGLMLQELHLSQNAINRISPDAWE
FCQKLSLDLTFNHLSRLDDSSFLGLSLNLTIHGNRVSYIADCAFRLSSLKTLDDLKNNE
ISWTIEDMNGAFSGLDKLRRRLILQGNRIRSIKKRAFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDCQLKWLPOWVAENNFSFVNASCAPQLLKGRSIFAVSPDGFWCD
DFPKPQITVQPETQSAIKGSNLNFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTVLETPSFLRPLLRTVKGETAVLQCIAGGSPPPKNWTKDDSPLVTER
HFFAAGNQLLIIVDSDVSAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLLLLDG
WATVGVVIIAVVCCVVGTSLVWVVIYHTRRNEDCSITNTDETNLPADIPSYLSQGTTLAD
RQDGYSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNVYGSDPFETYHTGCSPDPTVLMHYEPSYIKKKECYPCHPSEESERSFSNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGGCTGGCTTGCAAAAATG
AAGGATGCAGGACGCAGCTTCTCCTGGAACCGAACGCAATGGATAAAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTCTGTGAGCCCTGGATCTAACACAATGTGTATATGTGACACAGGGAGCATTCAAGAATGAAA
TAAACCAGAGTTAGACCGCGGGGTTGGTGTCTGACATAAAATAATCTTAAAGCAGCTGTTCCCCTCC
CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCAAAGAAAAAGTATGTCATTCTC
TATAAAGGAGAAAGTGAGCCAAGGAGATATTTGAATTCCCACAAGAGGAGAGGAAATTAAATAATACATCTGCAAAGAAA
TTTCAGAGAAGAAAAGTGTGACCGCGCAGATTGAGGCATTGATTGGGGAGAGAAACCAGCAGAGCACAGTTGGA
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGAGCTGGATTTCTTCATCAACCTCCTTTTTAAAT
TTTATTCCCTTGGTATCAAGATCATGCGTTCTCTGTTCTAACACCACCTGGATTCCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAACGTGTTGAATTCCAGAACACCCAGATAAATTATGA~~ATG~~TGAAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCTATTGACCCCTGCTTGTGGTCT
GCTGGCTCTCAACTCTGTGGTGGCTGGCTGGTGGCTCAGACCTGCCCTCTGTGTGCTCTGCAGCAA
CCAGTTCAAGGATGATTGTTGGAAAAACCTGCGTGGAGGTTCCGGATGGCATCTCCACCAACACAGGCT
GCTGAACCTCCATGAGAACAAATCCAGATCATCAAAGTGAACAGCTCAAGCACTGAGGCACTTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACCATGAAATTGGGGCTTCAATGGTCTGGCGAACCTCAACACTCTGGA
ACTCTTGACAACTCGTCTTAACCATCCGAATTGGAGCTTGTATACTTGTCTAAACTGAGCTGGCTCTGGTT
GCGAAACAACCCATTGAAAGCATCCCTCTTATGCTTTAACAGAAATTCCCTCTTGCGCCGACTAGACTTAGG
GGAATTGAAAAGACTTTCATACATCTCAGAAGGTGCTTGAAGGTCTGCCACTTGAGGTATTGAAACCTTGC
CATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAACATAGATGAGCTGGATCTTCTGGGAATCA
TTTATCTGCCATCAGGCCCTGGCTCTTCCAGGGTTGATGACACCTCAAAACTGTTGATGATACAGTCCAGAT
TCAAGTGATTGAAACGGAATGCCTTGACAAACCTTCAGTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAAC
ATTACTGCCTCATGACCTCTTCACTCCCTGCATCATCTAGAGCGGATACATTACATCACAAACCCCTGGAACTG
TAACTGTGACATACTGTGGCTCAGCTGGGATAAAAGACATGGCCCCCTGAACACAGCTTGTGCCCCGGTG
TAACACTCCCTCAATCTAAAGGGGAGGTACATTGGAGAGCTGACCAGAATTACTCACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAGGCATGGCAGCTGAGCTGAAATGTCGGGCTCCACATC
CCTGACATCTGTATCTGGATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAAGTGCAGGATAGCTGT
GCTCAGTGTGATGGTAAATTCAAAATGTAACTGTGCAAGATAACAGGCTATGACACATGTATGGTGAAGTAA
TTCCGGTGGGAATACTACTGCTTCAGCCACCCCTGAATGTTACTGCAGCAACCAACTACTCTTCTCTTACTTT
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGACGGACACAGATAACAAATGTGGGTCCCCACTCC
AGTGGTCAGTGGGAGACCAATGTGACCCCTCTCAGGATGAGGACGGACACAGATAACAGAGAAAACCTT
CACCACCCAGTGAATGATGAAACAGTGGGATCCAGGAATTGATGAGGTCTGAAGACTACCAAAATCATCAT
TGGGTGTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCAATTCTACAAGATGAGGAGACAGCACCA
TCGGCAAAACCATCACGCCAACAGGACTGTTGAATTATAATGTGGATGATGAGATTACGGGAGACACACC
CATGGAAAGCCACCTGCCCATGCCTGCTATGAGCATGAGCACCTAAATCAACTATAACTCATACAAATCTCCCT
CAACCACACAACAGTTAACACAATAATTCAATACACAGTTCACTGCATGAAACGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAAACAAACATCAAAAAAAA
GACAGTTTATTAACATGACACAAATGACTGGGCTAAATCTACTGTTCAAAAAGTGTCTTACAAAAAACAA
AAAAGAAAAGAAATTATTTATTAACATGACACAAATGACTGGGCTAAATCTACTGTTCAAAAAGTGTCTTACAAAAAACAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIICKVNSFKHLRHEILQLSRNHIRTIEIGAFNGLA
NLNTLELFNDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNADNLQSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHHNPWNCDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNVGN
TTASATLNVTAAATTTPFSYFSTVTETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYNNSYKSPFNHTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTCGGTTTCCCTCCTGCTGTTGGGGCA
TGAAAGGGCTCGCCGCCGGAGTAAAAGAAGGAATTGACCGGGCAGCGCAGGGAGGAGCGCCACGCACCGC
GAGGGCGGGCGTGCACCCCTCGGCTGGAAGTTGTGCGGGCCCCGAGCGCGCAGGGCTGGAGCTTCGGTAGA
GACCTAGGCCGCTGGACC CGCATGAGCGCGCAGCCTCCGTGCGCGCCGCGGGTTGGGCTGCTGTGC
GCGGTGCTGGGCGCGTGGCCGACAGCGCGTGCAGGGAAACTCGGGCAGCCCTCTGGGTAGCGCC
GAGGCCCATGCCCACTACCTGCCGCTGCCCTGGGACCTGCTGGACTGAGTCAGTCAGTCAGCGCTCTT
CCCAGCCACTCCCCTGGCTGGACTTAAGTCACAACAGATTATTTCATCAAGGCAAGTCC
ATGAGCCACCTTCAAAGCCTCGAGAAGTGAACAAACTGAACAAATGAATTGGAGACCATTCCAATCTGGACCA
GTCTCGCAAATATTACACTCTCCCTGGCTGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG
TTTCAGTCCCTGAAACCTTGGACCTTAGCAGCAACAATATTTCAGAGCTCAAACGCTCATTCCAGGCCACAG
CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGAACTGGTATTGACAATTGGCAACACA
CTCCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGTATCCCACCCAAGATGTTAAACTGCCCAACTGCAA
CATCTCGAATTGAAACCGAACAAAGATTAAAATCTAGATGGACTGACATTCCAAGGCCCTGGTCTGAGTCT
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAACATGGAAATTTTG
CAGCTGGACCATAACAAACCTAACAGAGATTACCAAGGGCTGGCTTACGGCTGCTGAGCTGGAGACCTCAT
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTCTGCCAGAAAGCTCAGTGAGCTGGACCA
ACTTCAATCACATTCAAGGTTAGATGATTCAAGCTTCTGGCTAACTTACTAAATACACTGCACATTGGG
AACAAACAGAGTCAGCTACATTGCTGATTTGCGCTTCCGGGGCTTCCAGTTAAAGACTTGGATCTGAGAAC
AATGAAATTCTGGACTATTGAAGACATGAATGGTGTCTTCTGGGTTGACAACACTGAGGGGACTGATACTC
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCAATTGGAGCATCTAGACCTGAGT
GACAACGCAATCATGCTTACAAGGCAATGCAATTCAAAATGAAGAAACTGCAACAAATTGCAATTAAATACA
TCAAGCCTTGTGCGATTGCCAGCTAAATGGCTCCCACAGTGGGTGGCGAAAACAACATTTCAGAGCTTGT
AATGCCAGTTGTGCCCATCCTCAGCTGCTAAAGAAGAACGATTTTGCTGTTAGCCCAGATGGCTTGTG
GATGATTTCCCAAACCCCAGATCACGGTTCAGCCAGAAACACAGTCGGAATAAAAGGTTCAAATTGAGTT
ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCAATGACTTTGCTTGGAAAAAAAGACAATGAACACTGCA
GCTGAAATGGAAAATTATGACACCTCCGGGCCAACGGTGGCAGGTGATGGAGTATACCACCATCCTTGGCT
CGCGAGGTGAAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCAAATCACTTGGTCATCCTACTCTGTC
AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATCAGCAAGACCCCCATGGATCTCACCCTCGAGCTGGGCC
ATGCCACGCTGGAGTGCTGCTGCTGGGGCACCCAGACCCCCAGATAGCCTGGCAGAAGGATGGGGCACAGAC
TICCCAGCTGCCAGGGAGAGACGGCATGCTGATGCCAGGGATGACCTGTTCTTATGTTGAGTGAAGATA
GAGGACATTGGGGTACAGCTGACAGCTCAGAAGACAGTGCAGGAAGTATTTCAGCAAATGCAACTCTGACTGTC
CTAGAAACACCATTTTGCAGGCTCATGCTGAGGGAGGAAACTGTAACCAAGGGAGAAACAGCCGCTTACAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACACTGGACCAAAAGATGATAGCCCATTGGTGTAAAGGAGGCAC
TTTTTGCAAGCAGGCAATCAGCTCTGATTATTGACTCAGATGTCAGTGATGCTGGAAATAACACATGTGAG
ATGCTAACACCTTGGCACTGAGAGAGGAAACCTGCGCTCAGTGTGATCCCCACTCAACCTGCGACTCC
CAGATGACAGCCCATCGTAGACGATGACGGATGGGCCACTGTGGGTGCTGATCATAGCCGTGGTTGCTGT
GTGGGGCACGTCACTGTTGGGGTGTACATATAACCACACAAGGGGGAGGAATGAAGATTGCAAGCATTACC
AACACAGATGAGACCAACTGCCAGCAGATTCTAGTTATTGTCATCTCAGGGAACTGACAGGCAG
GATGGGTACGTGCTTCAAGAAAGTGAAGCCACCACTGGTACATCTCAGGGCTGGATTTC
CAACATGACAGTACTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTT
CTTGTGCTGTTTGGGATCCACAGGCCCTATGTTGAAAGGGAAATGTGATGGCTCAGATCTTTGAAACA
TATCATACAGGTGCACTGCTGACCCAAGAACAGTTTAATGGACCACTATGAGCCAGTTACATAAAAGAAAAAG
GAGGCTACCCATGTTCTCATCCTCAGAAGAACAGTCTGCAAGGCCAGCTCAGTAATATATCTGTTGCTC
GTGAGGAAGCTTAACACTAGTTACTCTCAGAACATGAAGGACCTGGAAATGAAAATCTGTCAGTAAACAAGTCC
TCTTGTGTTTGTGCAAATCCAGAGCCAGCGTGGTTGCCCTGAGTAATTCTTCTATGGGTACCTTTGGAAAAA
GCTCTCAGGGAGACCTCACCTAGATGCTTCAAGCTTGGACAGCCATCAGATTGTCAGCCAAAGGCCTT
TTGAAAGCTCATCTTCCCAAGACTGGACTCTGGTCAAGGAAAGATGGAAAGAACAGATTTCAAGGAA
GAAAATCACATTGTACCTTAAACAGACTTAAAGGAAACTACAGGACTCCAATTTCAGTCTTATGACTTGGAC
ACATAGACTGAATGAGACCAAGGAAAGCTTAACACTACACTACCTCAAGTGAACCTTTATTAAAGAGAGAAC
CTTATGTTTAAATGGAGTTATGAAATTAAAGGATAAAATGCTTATTATACAGATGAACCAAATTAC
AAAAAGTTATGAAATTATACGGGAATGATGCTCATATAAGAATACCTTTAAACTATTTTAACTTT
TTTTATGCAAAAAGTATCTACGTTAAATTATGATATAAATCATGATTATTGATTTTATAATGCCAGA
TTCTTTTATGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCATTTTAAATAGAAGTT
ACTCATTATATTGCACTTAAATTAAATAAAATGTGCAATTGAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAEERPCPTTCRCLGDLDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRMNRISAIPPKMFKLPQLQHLELRNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMGAFWGGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC
QKLSLEDDLTFNHLSRLDDSSFLGLSLLNNTLHIGNNRVSYIADCAFRLSSLKTLDDLKNNEIS
WTIEDMNGAFSGLDKLRRLILQGNRIRSIKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQLQHLNTSSLCDQCLKWLQPQWAENNQSFVNASCAPHQLLKGRSIFAVSPDGVCDDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVAKLTNVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLDRVTKGETAVLQCIAGGSPPKLNWTKDDSPLVVTERHF
FAAGNQLLIIIVSDVDSDAGKYTCMSNTLGETERGNVRLSVIPTPTCDSPOQMTAPSLLDDGWA
TVGVVIIAVVCCVVGTSLVVVVIIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTIADRO
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKGNVYGSDFETYHTGCSPDPRTVLMHYEPSYIKKECYPCHPSEESCERSFSNISWPS
HVRKLLNTSYSNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLDGKERTDFQEENHICTFKQTLENYRTPNFQSYLDLT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTCGGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGGCCAGCCCGGGAGCGCAGCTGAGAC
TGGGGAGCGCGTTGGCCTGTGGGGCGCGCTCGGCGCCGGCGCAGCACAGGAAGGGGAAGCTGTGGCTGCC
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCCCCTGGGTGGTCCCCTATCCCTCTTATATA
GAAACCTCCACACTGGGAAGGCAGCGCGAGGCAGGGCTCATGGTGAGCAAGGAGGCCGCTGATCTGCAG
GCGCACAGCATTGGAGTTACAGATTTCAGATAACAAATGGAAGGCAGGAGGCAGAACAGCCTGCCGGT
TCCATCAGCCCTGGCGCCAGCGCATTGACTCGGCACCCCTGCAGGCACCATGCCAGGCCGGTGC
TGCTCTGCTGCTGCCACAGCTGCACCTGGACCTGTGCTTGCGTGGAGGCCAGGATTTGGCGAA
GTGGCGGCCACAGCTGAGCCCCGAAGAGAACGATTGCGAGGAGGAGCCGGTGTGGACTGAGCCCTGAGG
AGCCGGGCGCTGGCCAGCCCGTCACTGGGAGACTGTGCCGTGGACTGTG
GCGGTATTGACCTGCGTGAGTTCGGGGGACCTGCCTGAGCACACCAACCACCTATCTCTGAGAACAAACCAGC
TGGAAAAGATCTACCCCTGAGGAGCTCTCCCGCTGCACCGGGCTGGAGACACTGAACACTGCAAAACAACCGCCTGA
CTTCCCGAGGGCTCCAGAGAACGGCTTGAGCATCTGACCAACCTCAATTACCTGTACTTGCCAATAACAAGC
TGACCTGGCACCCCGCTCTCTGATCAGTGGAACCTTGCTGCCAATCTCACCAAGATCT
ATGGGCTCACCTTGGCCAAGCAAACCTTGAGGCTGTGACCTGCACAAACAACAGCTGGCAGACGCCGGC
TGCGGACAACATGTTCAACGGCTCCAGCAACGTGAGGCTCCTCATCTGTCCAGCAACTTCCCGCAGTC
CCAAGCACCTGCCGCTGCCCTGTACAAGCTGCACCTCAAGAACAAACAGCTGGAGAACGATCCCCGGGGC
TCAGCGAGCTGAGCAGCTGCGAGCTATACTGAGAACAAACTACCTGACTGACGAGGGCTGGACAACGAGA
CTTCTGGAAGCTCTCCAGGCTGGAGTACCTGGATCTGTCAGCAACACCTGTCTGGTCCAGCTGGCTGC
CGCGCAGGCTGGAGTACCTGCTGCTGCACAGCAACCAGCTGCCGGAGCAGGGCATCCACCAACTGGCTTCCAGGGC
TCAAGGGTTGACACGGTGCACCTGTACAACAAACCGCCTGGAGCGCTGCCAGTGGCTGCCTGCCGGTGC
GCACCCCATGATCCTGCACAACCAGATCACAGGATTGGCCCGAAGACTTGCACCCACTTCTGGAGG
AGCTCAACCTCAGCTACAACCGCATCACCAGCCCACAGGTGACCGCGACGCCCTCGCAAGCTGCCCTGCTGC
GCTCGTGGACCTGTCGGCAACCGGCTGCACACGCTGCCACCTGGCTGCCATGTAAGTCCATGTGTAAGG
TCAAGCGCAATGAGCTGGCTGCCATTGGACAGAGGGCGCTGGGGCATGGCTCAGTGCAGCTGAGCTGACCTCA
CCAGCAACCGACTGCGCAGCCAGCCCTGGGCCCCGTGCCCTGGTGGACCTGCCCATCTGAGCTGCTGGACA
TCGCGGGAATCAGCTCACAGAGATCCCGAGGGCTCCCCGAGTCACTTGAGTACCTGAGAACACA
AGATTAGTGCCTGGCCGCAATGCCCTCGACTCACGCCAACCTCAAGGGGATCTTCTCAGGTTAACAAAGC
TGGCTGGGCTCGCTGGTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAGGTCTGGACATTGAAGGCAACT
TAGAGTTGGTGAATTCCAAGGACCGTGGCCCTTGGGAAGGAAAAGGAGGAGGAGGAAGAGGAGGAGGAGG
AGGAAGAGGAAACAAAGATAGTGAACAGAGATGTGACATGTGACCTAGGATGATGGACCGCCGACTTTCTGC
AGCACACGCCCTGTGCTGTGAGCCCCCCTACTGCGCTGCACACAGAACACCCAGCTGCACACATGAGGCA
TCCCACATGACACGGCTGACACAGTCTCATATCCCCACCCCTCCCACGGCGTCCCACGCCAGACACATGC
ACACACATCACACCCCTAAACACCCAGCTGCCACACACAACCTACCCCTCCAAACCAACACAGTCTGTACAC
CCCCACTACCGCTGCCACGCCCTGTGAATCATGCAAGGAAGGGTCTGCCCTGCCACACACAGGCCACCA
TCCCCTCCCCCTGCTGACATGTGATGCGTATGCATACACACACACACATGCAAGTCATGTGCGAA
CAGCCCTCAAAGCTATGCCACAGACAGCTTGGCCAGCCAGAACATGCCATAGCAGCTGCCGTGCC
GTCCATCTGTCGGCTGGAGAACACAAGGGTATCCATGCTGTGGCAGGTGCTGCCACCCCT
GGAACCTACAAAAGCTGGTTTATTCTTCCATCTATGGGACAGGAGCCTCAGGACTGCTGGCTGCC
TGGCCACCCCTGCTCCTCCAGGTGCTGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCAGTTTCAAATGGCAAGGCCAGTGGAGGAGGATGGAGAGGCCCTGGGTGCTGCTGGGGCTTGGGG
CAGGAGTGAAGCAGAGGTGATGGGCTGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGAACACCTT
GTTCTCAGGCCTGTGGGGAGTTCCGGGTGCCATTATTTTATTCTTCTAAGGAAAAAAATGATAAAAT
CTCAAAGCTGATTTCTTGTATAGAAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAAA

FIGURE 108

MEGEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENEFEEEEPVVLVLSPEEPGPAAVSCPRDCACSGEQVVDCGGIDLREFPGDLP
EHTNHLSIQNNQLEKIYPEELSRLHRLETLNQNNRLTSRGLPEKAFEHLTNLNYLYLANNK
LTLPAPRFLPNALISVDFANYLTQIYGLTFGQKPQLRSVYLHNNKLADAGLPDNMFNGSSNV
EVILILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVTPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMILHNQITGIGREDFATTYF
LEELNLSYNRITSPOVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGFIFLRFNKLAVGSVVDASFRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGCGCGCGCAGCAGACCTGCTCCGGCGCGCCCTGCCGCTGTCTCCGGAGCGGCAG
CAGTAGCCCAGGGCGGGCTGGGGTTCTCGAGACTCTCAGAGGGCGCTCCCATCGGCACCACACCC
CAACCTGTTCTCGCGCCTCGCGTGCAGCCCCAGGACCCGCTGCCAACATGGATTTCCTGGCGTGGT
GCTGGTATCTCGCTCTACCTGCAGGGCGCCAGTTCGACGGAGGTGGCCAGGCAAATAGTGTATCGAT
TGGCTATGCTGTTATGGGGAGGATTGACTGCTGCTGGGCTGGCGTGGGACAGTGTAGCC
TGTGTGCCAACACAGATGCAAACATGGTGAATGATCGGGCAAACAAGTGAAGTGTATCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGGCCGTAAAGCACAGGTGATGAACACTTA
CGGCAGCTACAAGTGTACTGCTCAACGGATATATGCTCATGCCGGATGGTCTGCTCAAGTGCCCTGACCTG
CTCCATGGCAAACGTCAAGTATGGCTGATGTTAAAGGACAAATACGGTGCAGTGCCCACCCCTGGCCT
GCACCTGGCTCTGATGGGAGGACTGTTGATGAAATGTGCTACAGGAAGAGCCTCTGCCCTAGATT
TAGGCAATGTGTCACACTTTGGGAGCTACATCTGCAAGTGTATCGAAGGCTTCGATCTCATGTATAATGGAGG
CAAATATCAATGTATGACATAGACGAATGCTCACTGGTCAAGTGCAGCAGCTTGCTGATGTTATAA
CGTACGTGGGTCTACAAGTCAAATGTAAGAAGGATACCAGGGTATGGACTGACTGTTGATATCCAAA
AGTTATGATTGAACTTCAGGTCCAATTGATGACCAAAGGAAATGGTACCTTAAAGGGTGACACAGGAAA
TAATAATTGGATTCTGATGTTGGAAGTACTTGGCTCGAAGACACCATATACTCCCTATCATTACCAA
CAGGCCCTACTCTAAGCCAACAACAGACCTACACCAAAGGCCAACACCAAATTCTACTCCACCAACCCACC
CCTGCCAACAGAGCTCAGAACACCTTACCCACTACAACCCAGAAAGGCCAACACGGACTGACAACCTATAGC
ACCAGCTGCCAGTACACCTCCAGGGAGGATTACAGTTGACACAGGGTACAGACAGGACCCCTCAGAAACCCAGGG
AGATGTTGACTGTTCTGTTACAGGTTGAAATTTGACCATGGACTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCACTGGGAACCAATCAGGGACCCAGCAGGTGGACAAATATCTGACAGTGTGGCAGCCAAAGCCCCAGG
GGGAAAAGCTGACGGCTTGTGCTACCTCTGGCCCTATGCAATTGAGGGACCTGTGCTGCAATTGAGGCA
CAAGGTGACGGGGCTGCACTCTGGCACACTCCAGGTGTTGAGAAAACAGGTGCCACGGAGCAGCCCTGTG
GGGAAGAAAATGGGGCATGGCTGGAGGAAACACAGTACCTTGCAGGGGCTGACATCAAGAGCGAACATCACA
AAGATGATTAAAGGGTTGGAAAAAAAGATCTATGATGGAAAATTAAAGGAACGGGATTATTGAGCTGGAGAAG
AGAACACTGGGGCAAACATTGATGGTTTCAAGTATATGAGGGTTGGCACAGAGAGGGTGGCACCAGCTG
TTCTCCATATGCACTAAGAATAGAACAGGAAACTGGCTAGACTAGAGTATAAGGGAGCATTTCTGGCAGG
GGCCATTGTTAGAATACTTCATAAAAAAAGAAGTGTGAAATCTCAGTATCTCTCTCTCTTTCTAAAAAATTAGA
AAAAAATTGTCATTTAAGATGGTAAAGATGTTCTACCAAGGAAAGTAACAAATTATAGAATTTCCTAAA
AGATGTTTGATCCTACTAGTAGTATGCACTGAAATCTTAAAGTAACTAAATTGGACAAGGCTTAATTAGG
CATTCCCTCTGACCTCTAATGGAGAGGGATTGAAAGGGGAAGAGCCCACAAATGCTGAGCTCACTGAAATA
TCTCTCCCTATGGCAATCCTAGCAGTATTTAAAGAAAAAAGGAAACTATTTATTCCAAATGAGAGTATGATGGAC
AGATAATTAGTATCTCAGTAATGTCCTAGTGTGCGGTGTTCAATGTTCTCATGGTAAAGGTATAAGGCC
TTTCATTGTTCAATGGATGTTTCAGATTTTTTTTTTAAGAGATCCTCAAGGAACACAGTTGAGAG
ATTTCATGGGTGCAATTCTCTGCTTCTGTTGAGCAAGTTATCTGGCTGCTGAGAAAGAGTGCCCTGCC
ACACCGGCAGACCTTCCTCACCTCATCAGTATGATTGAGTTCTCTTCAATTGGACTCTCCAGGTCTCAC
AGAACAGTAATATTTTGAAACAATAGGTACAATAGAAGGTCTCTGTCATTTAACCTGGTAAAGGCAGGGCTGG
AGGGGAAAATAATCATTAAGCCTTGAGTAACGGCAGAATATATGGCTGAGATCCATTGTTAATGGTTCAATT
TCCTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGAAAATAATGAAAATTACTTTGATGCCAA
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTATTATTAATGTTT
CTAAAATAAAAATGTTAGTGGTTTCCAATGGCTAATAAAACAATTATGTAATAAAACACTGTTAGTAAT

FIGURE 110

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVVCQP
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRTCVDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDLMIYIGGKYQCHDIDECSLGQYQCSSFARCYNRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWI PDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTPERPTTGLTTIAPAASTPPGGITVDN
RVQTDPQKPRGDVFSLVHSCNFHDHGLCGWIREKDNDLHWEPIRDPAQQYLTVSAAKAPGG
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTTGCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACTTCCCTTGC~~AA~~CAGGTGCTCGGGCTGA
AGGTGACAGTGC~~C~~CATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTACCTACCCGTC
CACTATGGCTCCACACTCCAGCATCAGACATCCAGATCATGGCTATTGAGAGACCCC
ACAATGCCAAATACTTA~~C~~TGGCTGTGAATAAGTCTGTGGTCTGACTTGAATACC
AACACAAGTT~~C~~ACCATGATGCCACCC~~A~~TGCATCTGCTTATCAACCCACTGCAGTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTAGGGAA~~T~~GGA~~A~~CTCTATGCCAGTCA
GAAGATA~~C~~ACAAGTCACGGT~~G~~ATGATCCTGT~~C~~ACAAAGCCAGTGGTGCAGATTCA~~T~~CCTCCCT
CTGGGGCTGTGGAGTATGTGGGAACATGACCTGACATGCCATGTGG~~A~~AGGGGGACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGAC~~T~~GTCCACACCAGCTCCAC~~T~~ACTCCTTT
TCCCCAAAACAATACCTT~~C~~ATATTGCTCCAGTAACCAAGGAAGACATTGG~~A~~TTACAGCT
GCCTGGT~~G~~AGGAACCTGT~~C~~AGTGAA~~T~~GGAAAGTGATATCATTATGCCCATCATATATT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAGTAGGGGAAGT~~G~~TTACTGT
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAA~~G~~CATGGGC~~C~~CGCTTAGAAGTT
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAAACACATAAC
CGGCAGGCAAGATGAAACTCATTCACAGTT~~C~~ATC~~A~~CTCCGTAGGACTGGAGAAGCTG
CACAGAAAGGAA~~A~~ATCATTGT~~C~~ACCTTAGCAAGTATAACTGGAATATCACTATT~~T~~TGATT
ATATCCATGTGCTTCTTCCATGGAAAAAATATCAACCC~~T~~ACAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAACAGAACATCAGGAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTCGGAATATATGAATTGTTGCTTCCAGATGTTCTGGT~~G~~TTCCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGT~~G~~TATCGGGCAAGATTG~~C~~ACAGTACAGT
GTATGAAGTTATT~~C~~AGCACATCCCTGCCAGCAGCAAGACCATCCAGAGT**GA**ACTTT~~C~~ATGG
GCTAAACAGTACATT~~C~~GAGTGAA~~T~~CTG~~A~~AGAAACATT~~T~~TAAGGAAAACAGTGGAAAAGT
ATATTAA~~T~~CTGGAATCAGTGAAAGAAAC~~C~~AGGACCAACACCTCTTACTCATTATT~~C~~TTACA
TGCAGAATAGAGGCATTATGCAAATTGAA~~T~~CTGCAGGTTTCAGCATATA~~C~~ACAA~~T~~GT~~T~~
GTGCAACAGAAAACATGTTGGGAA~~A~~ATT~~C~~CTCAGTGGAGAGTC~~G~~TTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGTT~~C~~CTCATAGTTGT~~T~~ATGAA~~A~~ATATCTACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAAACTTACATTGTTG~~C~~ATT~~T~~T~~C~~AGCAGACTTGT~~T~~TATTAAATT~~T~~TATTAGTG
TTAAGAATGCTAAATT~~T~~ATGTTCAATT~~T~~TATT~~C~~AAATT~~T~~CTATCTTGT~~T~~ATTGTACAA
CAAAGTAATAAGGATGGTTGT~~C~~ACAAAACAAA~~A~~CTATGCCTCTTTTTCAATCACC
AGTAGTATT~~T~~TGAGAAGACTGTGAACACTTAAGGAA~~A~~GTACTATTAAAGT~~C~~TTATT~~T~~TA
TTTTTTCAAGGAAAGATGGATTCAAATAATTATTCTGTTTGCTTTAAAAA~~AAA~~AAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLSASQ
KIQVTVDDPVTKPVVQIHPHPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPTEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGC~~GA~~**AATGGCGCCCTCCGGGAGTCTTGCAGTTC**CCCTGGCAGTCCTGGTGTGTT
GCTTGGGGTGTCTCCCTGGACGCACGGGCGGCCGGAGCAACGTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTATGCCCGTGGTGCCTGCT
TGTCAAAATCTTCAACCGGAATGGAAAGTTTGCTGAATGGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCTACTATTTATCATTGTAAGATGGTGAATTAGGCCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAAACTTATAAGTGTAAAGAGTGGAAAGAGTATTGAGGCCGTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCAGTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTATTGAAGACCTGGATTGCCAGTGTGGGATCATATACT
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC
AGATTGCCTTGTCTCAAAAAGGCGCAGACCACAGCCATAACCCATAACCCCTCAAAAAAAT
TATTATCAGAACATCTGCACAACCTTGAAAAAAGTGGAGGAGGAACAAGAGGGCGGATGAAGAA
GATGTTTCAGAAGAAGAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAACATGC
CATAAAGACAAACGCTCTGGGCCATCATTGCCACAGATAAATCCTAGTTAAATTTATAG
TTATCTTAATATTGATTTGATAAAACAGAACAGATTGATCATTGTTGGTTGAAGTG
AACTGTGACTTTTGAAATATTGCAAGGTTCAAGTCTAGATTGTCATTAATTGAAGAGTCTA
CATTAGAACATAAAAGCACTAGGTATAACAGTTGAAATATGATTAAGCACAGTATGATG
GTTTAAATAGTTCTCTAATTTGAAAAATCGTGCCAGCAATAAGATTATGATATTGTT
TTAATAATAACCTATTCAAGTCTGAGTTGAAAATTACATTCCCAGTATTGCAATT
TGAGGTATTTAAGAAGATTATTTAGAGAAAAAATTCTCATTTGATATAATTCTCTG
TTTCACTGTGAAAAAAGAACAGATATTCCCATAAATGGGAAGTTGCCATTGTCTCAAG
AAATGTGTTTCAGTGACAATTCTGTTCTTTAGAGGTATATTCCAAAATTCTCTG
ATTTTAGGTTATGCAACTAATAAAACTACCTTACATTAATTACAGTTCTACACA
TGGTAATACAGGATATGCTACTGATTAGGAAGTTTAAGTTCATGGTATTCTTGTGATTC
CAACAAAGTTGATTTCTTGATTTCTTACTTACTATGGGTTACATTTTTATT
CAAATTGGATGATAATTCTTGAAACATTTTATGTTTAGTAACAGTATTCTTGT
GTTTCAAACGTAAAGTTACTGAGAGATCCATCAAATTGAACAATCTGTTGTAATTAAAATT
TTGCCACTTTTCAGATTTCACATCATTCTGCTGAACCTCAACTGAAATTGTTTT
TTCTTTGGATGTGAAGGTGAACATTCTGATTTGTCTGATGTGAAAAAGCCTGGTA
TTTACATTGAAAATTCAAAGAACGTTAATATAAAAGTTGCTACTCAGGAAAAAG
CATCTTCTGTATATGCTTAAATGTATTGTCCTCATATAACAGAAAGTTCTTAATTGAT
TTTACAGTCTGTAATGCTGATGTTAAAATAAACATTATTATAATTAAAAGACAA
ACTTCATATTATCCTGTTCTTCTGACTGGTAATATTGTGTGGGATTTCACAGGTAAAA
GTCAGTAGGATGGAACATTAGTGTATTCTACTCCTAAAGAGCTAGAACATAGTTT
CACCTTAAAGAACGGGGAAATCATAAAACAAATGAATCAACTGACCATTACGTAGTAGAC
AATTCTGTAATGTCCCCTCTTAGGCTCTGTTGCTGTGAATCCATTAGATTACAG
TATCGTAATATACAAGTTCTTAAAGCCCTCTCCTTAAAGAACATTCCTAAGCACAAACCT
AAAGAGTTGGATGTGTAACCTGATGCCCTAGAAAAATATCCTAAGCACAAACCT
TTCTAACCAACTCATTAAAGCTGAAAAAAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIIFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSMSALFQLSMWIRTCNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNPAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCGAGTGTCCAGCTGGGAGACCCGTGATAATTGTTAACTAATTCAACAAACGGGACCCTT
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGACAGGCAGATTGGAAGAGCGGG
AAGGTCTGGCCAGAGCAGTGTGACACTTCCCTCTGTGACC**ATGAAACTCTGGGTGTCTGC**
ATTGCTGATGCCCTGGTTGGTGTCTGAGCTGTGAGCTGGCAGGCCAATTCTCACCTCTATTG
GGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTCAGTCTGTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAAGAGCTGGGCCAACAAAATGGAAGCCTTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCCGTGAATGCCTACAAACTGG
TGAAGCGGCTAACACACAGACTGCCCTGCCCTGGAGGACCTGTCCTGCAGGACTCAGCTGCA
GGTTTTATGCCAACCTCTGTGAGCGGGCAGTTCTCCCCACTGATGAGGACGAGATAGG
AGCTGCCAACGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA
GAGGGGAACCTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG
GGCCGCTCGGCCTACAATGAAGGGACTATTATCATACGGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGTGATGCCGGGGAGGAGGCCACCAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGCTTCCAGTTGGGTGATCTGCACCGTGCCTGGAGCTCACCCGCCGCTGCTC
TCCCTGACCAAGCCACGAACGAGCTGGAGGAATCTGCCGTACTTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCCAGAAGGCA
TCTATGAGAGGGCTGTGGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTGTGCTGGG
GAGGGTGTCAAACACTGACACCCCGTAGACAGAAGAGGGCTTCTGTAGGTACCACCATGGCAA
CAGGGCCCCACAGCTGCTCATGCCCTTCAAAGAGGAGCAGGAGTGGACAGCCCGCACA
TCGTCAAGGTACTACGATGTCATGTCATGAGGAAATCGAGAGGATCAAGGAGATCGAAAAA
CCTAAACTTGCACGAGCACCGTCTGTGATCCCAAGACAGGAGTCCTCACTGTCGCCAGCTA
CCGGGTTCCAAAAGCTCTGGCTAGAGGAAGATGATGACCCCTGTTGGCCGAGTAAATC
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCGAGAATTGTTACAGGTTGCAAAT
TATGGAGTGGAGGACAGTATGAACCGCACTCGACTTCTAGGCGACCTTTGACAGCGG
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTGCGGAGCGGGGAAGGTGACTACCGAACAGACATGCTGCCTGCC
TGTGCTTGTGGCTGCAAGTGGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT
TGAGACCTGTGGATCAACAGAAGTTGACT**GA**CATCCTTCTGTCCCTCCCTGTC
CTTCAGCCCATGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGGACTCCTGT
GTGACTGAAGTCCCAGCCCTCATTGAGCCTGCCCCAAGGCTAGGATCA
AAAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCAAGTGAACCAAAGTTCTGATACCTGTTACATGTTGTTTAT
GGCATTCTATCTATTGTGGCTTACCAAAAATAAAATGTCCTACCAAGAAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIWSA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGEPLPGTKYQAMLSVDDCFGMGRSAYNEGDDYYHTV
LWMEQVLKQLDAGEEATTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVDFYLPERDVYESLCRGEGVKLTPRRQKRLF
CRYHHGNRAPQOLLIAPFKEEDEWDSPHIVRYYDVMMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKGTAVFWYNLLRSGEGDYR
TRHAACPVLVGCKWVSNKFHERGQEFLRPCGSTEV

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTCCTCCTTTAGTGGAAACAGACCCATAATCCCAGTGTGAGTGAAATTGATTGT
TTCATTTATTACCGTTGGCTGGGGTTAGTTCCGACACCTTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA
AGACAGGACAATCTTCTTGGGGATGCTGGTCCTGGAAGGCCAGCGGGCCTGCTCTGCTTTGCCCTATTGACCC
CAGGTTCTCTGGTTAAAAGCTACTACTGGCCTGGGCCATCAATCATTGATCCTTGAGGCTGTGCC
CCTGGGGCACCCACCTGGCAGGGCCTACCACCATATGCAGTGCAGCTCCCTGTTGGCTCTGCTGCCAGCGCTTC
CCCTCATCTTAGGGCTGTCTCTGGGGTGCAGCCTGAGCCTCTGCGGGTTCTGGATCCAGGGGAGGGAGAAG
ATCCCTGTGTCGAGGCTGTAGGGGAGGCCAGAATCCAGATTGAGAGCTGGCTAGACCAAAGTG
ATGAAGACTCAAACCCGGATTGTCCTACTACAGGGACCCAAACAAGCCCTACAAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGAGCTGGCTCCCGTGAGCGGTTGCTGGCTGACCTCCCGAGCTACACTGTCCA
CTTGCGCGTGGCTGTGAACCGTACGGTGGCCCATCACTTCCTCGGTTACTCTACTTCAGTGGCAGCGGGGG
CCCAGGCTCCAGCAGGGATGCAAGGTGGTGTCTCATGGGATGAGCGGCCGCTGGCTATGTCAGAGACCCCTGC
GCCACCTTCACACACACTTGGGCCACTACGACTGGTCTCATCATGCAAGGATGACACATATGTGCAAGGCC
CCCAGGCTGGCAGCCCTGCTGGCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGCAGAGGAGTTCAATTG
GCGCAGGCAGCAGGGCCGGTACTGTCACTGGGGCTTGGCTACCTGTTGTCACGGAGTCTCTGCTTCGTC
GGCCACATCTGGATGGCTGCCAGGAGACATTCTCAGTGGCCCTGCAAGCAGGCTTGGACGCTGCCTCATTTG
ACTCTCTGGCGTGGCTGTCTCACAGCACAGGGGAGCAGTATGCTCATTTGAACTGGCCAAAAATAGGG
ACCCCTGAGAAGGAAGGGAGCTGGCTTCTCTGAGGTGCTGGCTGGGACTACTTCACAGAGCACACCTCTCCTGTGCA
ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCGGGCTTACAGTGAATAGAACAACTGCAGGCTCAGA
TCCGGAACCTGACCGTGCCTGACCCCCGAAGGGGAGGGCAGGGCTGAGCTGGCCGTTGGGCTCCCTGCTCCTTCA
CACCAACTCTCGCTTGAGGGTGTGGACTACTTCACAGAGCACACCTCTCCTGTGCAAGATGGG
CTCCCAAGTGCCACTACAGGGGCTAGCAGGGGGACGTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA
ATCGGGCTATCAGCCCCGCTGCGCTTCCAGAACGCAGCAGACTGCTCAACGGCTATCGGCGCTCGACCCAGCAC
GGGGCATGGAGTACACCCCTGGACCTGCTGTTGGAATGTGTGACACAGCGTGGCACCAGGGCCCTGGCTCGCA
GGGTCAAGCTGCTGCCACTGAGCGGGTGGAAATCTACCTATGCCCTATGTCAGTGGCCACCCAGTGC
AGCTGGTGTGCCACTCTGGTGGCTGAAGCTGCTGCAGCCCCGTTCTCGAGGCGTTGCAAGGCAATGTCC
TGGAGCAGAGAACATGCAATTGCTACCCCTGTTGCTGGCTACGGGCCACGAGAACGGTGGCGTGGAGCTCCAG
ACCCATTCTGGGGTGAAGGCTGCAGCAGCGGAGTTAGAGCGACGGTACCCCTGGGACGAGGCTGGCCTGGCTCG
CTGTGCGAGCAGAGGCCCTTCCAGGTGCGACTCATGGACGTGGTCTGCAAGAACGACCCCTGGGACACTCT
TCTCCCTTACCCAGTGGACAAGGCCCTGGGCCAGTCTCAACCGCTGTCGATGAATGCCATCTCTGGCT
GGCAGGGCTTCTCAGTCATTCCAGGAGTTCAATCTGCCCTGTCACCACAGAGATCACCCCCAGGGCCCC
CGGGGGCTGGCCCTGACCCCCCTCCCCCTGGTGTGACCCCTCCGGGGGCTCTATAGGGGGAGATTG
ACCGGCAGGCTTCTGCGGAGGGCTGTTCTACAACGCTGACTACCTGGGGCCGAGCCCGGCTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGGCCCTGGAGGGCTGGAGGGTGTGGATGGATGTTCTCCGGTCTCAGGGCTCC
ACCTCTTCCGGCGTAGAGGCCAGGGCTGGTGCAGAACAGTTCTCCCTGCCAGACTGCCAGCCCACGGCTCAGTGAAG
AACTCTACCAACCGCTGCCCTCAGCAACCTGGAGGGCTAGGGGCCGTGCCCAGCTGGCTATGGCTCTTTG
AGCAGGAGCAGGCCAATAGCACTTAGCCGCCTGGGGCCCTAACCTCATTACCTTCTGGCTCTGCC
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTAAATGAAAATGTTATTAA
ACATGCTTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDZRARLD
QSDEDFKPRIVPYYRDPNPKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFYLLSRSLLRPHLDGCRG
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGGEAGLSWPVGLPAPFTPNSRFEV
LGWDYFTEQHTFSCADGAPKCPHQASRADVGDALETALEQLNRRYQPRLRFQKQRLLNGYR
RFDPARGMEYTLDLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLPLL
VAEAAAAPAFLEAFAANVLEPREHALLTLLVYGPREGGRGAPDPFLGVKAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPGPEVLRCRMNAISGWQAFFP
VHFQEFPALSPQRSPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEAELEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRALAMALFEQEQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGC~~CCAACGTGAGAGGAACCCGTGCGCGCTGCGCTTCCTGTCCCCAAGCC~~
GTTCTAGACGCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTATGCTTGG
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTTGTAAAACC
CAAAGATGTGAGTCTTGGGCTGCAGTAAAGGAGACTTGGACCAACACTGTGACAAAGCAG
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCAATTAAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACA
GTTCTCCTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAACCAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC
CAACCAGGTAGTAGAAGGCTGTTCTAGATATGGCTGTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGTATGGGTATACCGCCTAGGGCATTGGCATATTTCAAT
GATGCATTGGTTTCTTACCTCAAATGGTCTGACAATGACTTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTGTTGTCATTATTGAGTAGTAACATATCCAA
TACAGCTGTATGTTCTTTCTTCTAATTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTAACATGGGTGGTTTTCTTAAAACACATGAACATTGAAATG
TGGTGGAAAGAAGTGTAAAGAATAATAATTGCAAATAACTATTAAATAATTATAT
GTGATAAAATTCTAAATTGAAACATTAGAAATCTGTGGGCACATATTGCTGATTGGTT
AAAAAATTAAACAGGTCTTACCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAAACCTTCTAGCTGTGTGTTCCCTTACTTCTAATACTGATTATGTTCT
AAGCCTCCCCAAGTCCAATGGATTGCCTCTAAAATGTACAACTAAGCAACTAAAGAAA
ATTAAAGTGAAGTGGAAAAT

FIGURE 120

MLSSESSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKFESINMDTNMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKDPSPQFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCACCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAAACAAAAACCAAAGAGAGAGAAAAATGAATTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTCTTCCAAATGTTCTATGGACTGTTGCT
GGGATCCCCATCCTATTCTCAGTCGCTGTTCATCACAGATGTGTTGTGACATTCGCAT
CTTCAAACCTGTGATGAGAAAAAGTTCTAGCTACCTGAGAATTCACAGAGCTCCTGCT
ACAATTATGGATCAGGTTCAAGAATTGTTGCCATTGAACGGAAATTTCAATCC
AGCTGCTACTCTTTCTACTGACACCATTCTGGCGTTAAGTTAAAGAACTGCTCAGC
CATGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCTTCTACAAGA
AACCTAAAATGAGAGAGTTTTATTGGACTGTCAGACCAGGTTGTCAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTGACAAAGTCTCTGAGCTCTGGATGTAGGGAGGCCAACAA
CATAGCTACCCTGGAGGACTGTGCCACCATGAGAGACTCTCAAACCCAAGGCAAATTGGA
ATGATGTAACCTGTTCTCAATTATTCGGATTGTGAAATGGTAGGAATAATCCTTG
AACAAAGGAAAATCTCTTTAAGAACAGAAGGCACAACTCAAATGTGAAAGAAGGAAGAGCA
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTGTGCGCTGAACCTCAAAGGACTTC
ATAAGTATTTGTTACTCTGATAAAATAAGTAGTTAAATGTTAAAAAAAAAAAAAAA
AAA
AAAAA

FIGURE 122

MNSSKSSETQCTERGCFSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCNYGSGSVKNCCPLNWEYFQSSCYFFSTDТИSWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLEDATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCCGCCGCTGCCGCTGGCCCCCTCAGCAACCTCGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTCGCGCTCGGCTGCCGACTCTTCTGCTGCTGCTTTCAAGGGGCTGCCTGATAGGGCTGAAATC
TCAAATCCAGCAATCGAACCCCAGTGGTACAGGAATTGAAAGTGTGGAACGTGCTGCACTATTACGGATTGCG
AGACAAAGTGACCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTGACAACAAAAA
TTCAGGGAGACTTGGCGGGCTGTCAGAAAATCTGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTAGGTCGTTGCTGAAATGACCGAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAAGCCAGTGACCCCTGCTGTAGAGTGCCGAAGGCTGTACCAAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCACCCCCGGCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT
CCAGAGCCAATCCAGATTCGCAATTCTCTTCACTTAAACTCTGAAACAGGCACTTGGTGTTCACTGCTG
TTCACAAGGACGACTCTGGCAGTACTACTGCATTGCTTCCAATGACGCAAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGTCTGGTGTCTGCTGACTGCCCTGA
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACCAAGATGGAGTTAACTACATCCGCACTGACCGAGGAGGGCACTTCAGACACAAGTCATGTTG
TGATCTGAGACCCCGGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTC
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTCAGAAGCTTTCGTTGGCCAAGTTGACCA
CTACTCTCTTACTCTAACAGCCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAATAACACACAA
GGAAGCGAACATGGGTGGTCACTGAGTTGGGTTCTAATCTGTTCTGGCTGATTCCCGCATGAGTATTAGG
GTGATCTTAAAGAGTTGCTACGTAAACGCCCCGTCTGGGCCCCGTGAAGCCAGCATGTTACCAACTGGTCGTT
CAGCAGCCACGACAGCACCATGTGAGATGGCAGGGTGGCTGGACAGCACAGCAGCGCATCCGGCGGAAACCCA
GAAAAGGCTTCTAACAGCAGCCTTACTTCATCGGCCCACAGACACCACCGCAGTTCTTCTAAAGGCTCTGC
TGATCGGTGTGCACTGTCATTGAGAAAGCTTTGGATCAGCATTGTTGAAACAAACAAAAATCAGGAAG
GTAAATTGGGTGCTGGAAGAGGGATCTGCTGAGGAACCTGCTGTCACAGGGTGTCAAGGATTTAAGGAAA
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTCTATGGGTCTGTTTATTAAATTT
TACATCTAAATTGGTCTAACAGGATGTATTGATTGAAAGAAAATTCTATTAAACTGAAATATATTGT
CATACAAATGTTAAATAACCTATTGTTAAAAAGGTTCAACTTAAGGTAGAAGTTCAGCTACTAGTGTAAAT
TGGAAAATATCAATAATTAGAGTATTGTTACCAAGGAATCCTCTCATGGAAGTTACTGTGATGTTCTTTCT
CACACAAGTTTACGCTTTTCAAAAGGAACCTACATGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAATTCCAGTTAACAGCAATGTTGAAATCAGTTGCATCTCTCAAAAGAAACCTCTCAGGTTAGCTTGAAC
GCCTCTCTGAGATGACTAGGACAGTCTGACCCAGAGGCCACCCAGAACGCCCTCAGATGTACATACAGATG
CCAGTCAGCTCTGGGTTGCCAGGCCAGGCCGCTCTAGCTCACTGTCAGCTGCCCTGCTGCCAGGAGGCCCT
GCCATCCTGGGCCCTGGCAGTGGCTGTCCAGTGAGCTTACTCACGTGGCCCTGCTCATCCAGCACAGC
TCTCAGGTGGCAGTCAGGACACTGGTGTCTCATGTAGCGTCCAGCTTGGCTCTGTAACAGACCTCT
TTTGGTTATGGATGGCTCACAAAATAGGGCCCCAATGCTATTGTTTTAAGTTGTTAATTATTGTT
AAGATTGTCTAACGGCAAAGGCAATTGGCAAATCAAGTCTGTCAGTACAATAACATTAAAGAAAATGGAT
CCCACGTCTCTTGCACAGAGAAACGACCCAGACGCCACAGGCTCTGTCATTTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCCCTGGGGGGAGGAAAG
TGAAAACGCCCTAACAGCAGTTCTAATTGACTTTAACATTGTCATCCGCCAGAACACTGCTCCCATT
TGTGGGGGGACATTAGCAACATCACTCAGAACGCTGTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
GCCGTGCTGGACTCAGGACTGAAGTGTGAAAGCAAGGAGCTGAGAAGGAGCACTCCACTGTGCTGCC
GAATGGCTCTCAACTCACCTTGCTTTCAGCTTCAGCTCAGTGTCTGGGTTTTTATACTTTGACAGCTTTTT
AATTGCAACATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGCAGGCCAGGCCCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC
CCTCCATCATTGCCACCTGGTAGAGAGGGATGGCTCCCCACCTCAGCGTTGGGATTTCAGCTCCAGCCCT
TCTTGGTTGTCAGTGATAGGGTAGCCTTATTGCCCTCTTCTTATACCCCTAAACCTCTACACTAGTGCA
TGGGAACCCAGGTCTGAAAAGTAGAGAGAAGTGAAGTAGAGCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTAAAGATATGAATGTGACTCAAGACTCGAGGCCATACGAGGCTGTGATTCT
GCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAAC
CTCATTATAAAAGCTTACAAAAACCCA

FIGURE 124

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAHKDDSGQYYCIASNDAGSARCEEQEMEVYDNLIGGIIGG
VLVVLAVALALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267